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Title:
Perfect score:
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seq length: 2000000000
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A_Geneseq_29Jan04:*
1. geneseqp1980s:*
2. geneseqp1990s:*
3. geneseqp2000s:*
4. geneseqp2001s:*
5. geneseqp2002s:*
6. geneseqp2003as:*
7. geneseqp2003bs:*
8. geneseqp2004s:*
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916
1 MDVTTQHPWFKRTLGPFYPS......HAERAIPVSREEKPTSAPSS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          September 27, 2004, 13:16:53; Search time 54 Seconds (without alignments) 905.198 Million cell updat
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                                                                                                                                                                                                                                                                                                                                           1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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geneseqp2002s:*
geneseqp2003as:*
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geneseqp2004s:*
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ㅂ. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

SUMMARIES

			28	30	20				16			13			_	9			σ			ω	2	-	1	Result
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ADE75363	ADE83437	AA018753	ABB78997	ABB60738	AAG03888	ADES6085	ABG93942	AAR78693	AAY60544	ADE75368	ABP43873	ABG93941	AAB42472	AAR78692	ADB99861	ABM04835	AAR87512	AAG03887	ADE75367	ADE56087	AAG03886	AAY07074	ABG76084	ADE75366		
Ade75363	Ade83437	Aao18753			Aag03888				Aay60544	Ade75368	Abp43873	Abg93941	Aab42472			-	Aar87512	Aag03887	Ade75367	Ade56087	Aag03886	Aay07074	Abg76084	Ade75366	Description	
	Human Pro	Human HSP	Human HSB	Drosophil	Human sec		Rat polyp	Rat skele						Human ske	Mouse alp	Rat alpha	Human alp	Human sec				Renal can	Human chi	Human sHS		

289.5 31.6 459 5 ABG94499 289 31.4 205 2 AAR41022 288 31.4 471 2 AAR41022 288 31.4 471 2 AAR41022 288 31.1 102 5 AAU99185 283 30.9 232 3 AAB11397 283 30.9 232 4 AAB774198 283 30.9 232 4 AAB772019 276 30.1 182 4 AAB70768 283 30.9 232 4 AAR722019 276 30.1 182 4 AAB70778 265.5 29.0 136 5 ABG93940 265.5 29.0 136 5 ABG93940 265.5 29.0 136 5 ABG93967 271 234 23.4 186 4 ABB60677 202.5 22.1 208 4 ABB60679 193 21.1 199 4 ABB60679 174.5 19.1 445 4 ABB60679	31.6 459 31.4 205 7 31.4 471 2 31.1 4 471 2 31.1 4 471 2 31.1 102 5 30.9 232 4 30.9 242 4 30.9	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	
.6 6 459 .6 2006 .7 20	.6 459 5 ABG94499 .6 206 7 ADE83435 .4 205 2 AAR41022 .4 471 2 AAW54352 .4 471 2 AAW54352 .4 471 5 ABU04599 .1 102 5 AAU99185 .9 232 3 AAB11397 .9 232 4 AAB70768 .9 232 4 AAB70768 .9 232 4 AAB70768 .9 232 4 AAB70768 .9 232 6 AAW72019 .1 182 5 ABG93940 .0 136 5 ABG93940 .0 108 4 ABB60677 .1 208 4 ABB60477 .1 208 4 ABB60479 .1 199 4 ABB60479 .1 199 4 ABB60467	174.5	193	196	202.5	214	238	265.5	266	276	283	283	283	283	284.5	288	288	288	289	289.5	
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ABG94499 ADE83435 AAR41022 AAW54352 AAW99185 AAB104599 AAU99185 AAB777198 AAB7772019 ABU72916 ABG93940 AAR05780 AAR05780 AAR05780 ABB60477 ABB60477 ABB60477 ABB60477		4	4	4	4	4	7	N	ហ	4	4	4	4.	ω	5	9	N	N	7	ഗ	
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RESULT 1 ADE75366 ADE75366 standard; protein; 173

ALIGNMENTS

Human sHSP family member, alphaA-crystallin. 29-JAN-2004 ADE75366; (first entry)

Hybrid protein chaperone; protein stabilisation; heat shock protein; sHSP family; protein aggregation inhibition, cell death inhibition; genome stability pathway inhibition; protein denaturation identification; protein conformation related disease; cardiomyopathy; cataract; neurodegenerative disease; cardiant; ophthalmological; neuroprotective; gene therapy; alphaA-crystallin; human.

Homo sapiens

WO2003091266-A2

06-NOV-2003.

23-APR-2003; 2003WO-GB001721.

23-APR-2002; 2002GB-00009334.

(UYDU-) UNIV DUNDEE

Quinlan R;

WPI; 2003-865571/80.

New hybrid protein chaperone (e.g. heat shock protein) useful for stabilizing proteins and/or protein activities, or as an agent to prevent protein aggregation, or for treating diseases involving altered protein

Disclosure; Fig 11; 45pp; English.

The invention relates to a hybrid protein chaperone for stabilising proteins and/or protein activities. Protein chaperones (also known as heat shock proteins) are divided into 4 families on the basis of their primary sequence and chaperone properties: HSP90, HSP70, HSP60 and sHSP (small heat shock protein). The invention is based upon the finding that among the sHSP family, which have a general structure of a central domain (called the alpha-crystallin domain) flanked by N and C-terminal regions. regions o H

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RESULT 2
ABG76084
ID ABG7
XX ABG7
XX ABG7
XX ABG7
XX Humm
XW Humm
XW Inc.
XW Inc.
XW inc.
XW inc.
XW alp.
XX ABG7
XX EMM
XM FFT Reg
FT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; crystallin; chimeric; alpha BNAC crystallin; protein shelf life; protein aggregation; accessible hydrophobic region increase; mutant; larger size oligomer formation; intersubunit interaction increase; larger aggregate formation; larger porous oligomer formation; increased ellipticity; less solvent accessible tryptophan; mutein; increased chaperone-like activity; alpha A crystallin; alpha B crystallin.
                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human chimeric protein alpha BNAC crystallin
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                                                                                                         US2002177192-A1
                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL
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                                                                                                                                                                                                              /note= "Alpha B crystallin N-Terminal"
83. .177
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                          'note= "Alpha A crystallin C-Terminal"
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99.4%;
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Pred. No. 4.3e-97;
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28-NOV-2002

15-JUL-1998; 28-JAN-1999.

98WO-US014679

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  larger size oligomers, shows an increase in intersubunit interaction, forms larger aggregates, forms larger porous oligomers and shows increased ellipticity as compared to eye lens crystallins alpha A and alpha B. The tryptophan residues in the polypeptide are less solvent accessible as compared to those of eye lens crystallins alpha A and alpha B. The polypeptide shows extraordinarily high chaperone-like activity ranging between 3 - 6 times that of the eye lens crystallins alpha A and alpha B. The present sequence represents the amino acid sequence of the human alpha BNAC crystallin chimeric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a chimera alpha BNAC polynucleotide that encodes a chimeric alpha BNAC polypeptide. The polypeptide is useful for preventing protein aggregation. The polypeptide is also useful for increasing the shelf life of proteins of pharmaceutical value. The polypeptide shows an increase in accessible hydrophobic regions, forms
                                                                                                                                              Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimera alpha BNAC nucleic acid, useful for preventing aggregation of proteins and also for increasing shelf life of proteins of pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                  WO9904265-A2
                                                                                                  Homo
                                                                                                                               prostate cancer.
                                                                                                                                                                                               Renal
                                                                                                                                                                                                                                02-JUL-1999
                                                                                                                                                                                                                                                              AAY07074;
                                                                                                                                                                                                                                                                                             AAY07074 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 10; 17pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumar LVS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2001; 2001US-0279223P.
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                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                               cancer associated antigen precursor sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX12062.
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                                                                                                                                                                                                                                                                                                                                                                             RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS 177
                                                                                                                                                                                                                                                                                                                                                                                               RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                            WFDTGLSEMRLEKDRFSVNLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDIAIHHPWIRRPFFPFHSPSRLFDQFFGEHLLESDLFP-TSTSLSFFYLRPPSFLRAPS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQ--SLFR--T 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.6%;
77.0%;
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                                                                                                                                                                                                                                                                                               175
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Pred. No. 3.5e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 177;
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                                                                                                                                              lung cancer;
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RESULT 4
AAG03861
ID AAG0
XX AAG0
XX D6-C
XX D6-C
XX Huma
XX Huma
XX Gene
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Best Local S
Matches 97
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10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                    06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated cancer associated nucleic acids and using sera from cancer patients, used to develop diagnosis, monitoring or treatment of cancers.
                                EP1033401-A2
                                                             Homo sapiens
                                                                                                                                                                                                                                  AAG03886 standard; protein; 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-132448/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1998;
                                                                                          therapy;
                                                                                                                                                                                                                                                                                                                                            116
                                                                                                                                                                                                                                                                                                            120 RKYRIPADVDPLTITSSLSSDGVLTVNGPRKQ----VSGPERTIPITREEKPAVTAAP 173
                                                                                                                                         secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MDIAIHHPWIRRPFFFFHSPSRLFDQFFGEHLLESDLFP-TSTSLSPFYLRPPSFLRAPS
                                                                                                                                                                                                                                                                                                                                         RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP--TSAP 171
                                                                                                                                                                                                                                                                                                                                                                           WFDTGLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFH 119
                                                                                                        EST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA:
                                                                                                                                                                    (first entry)
                                                                                        chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00896164.
97US-0061599P.
97US-0061765P.
97US-00948705.
97GB-00021697.
                                                                                                                                       protein, SEQ ID NO: 7967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INST
                                                                                                     expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00102322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , <sup>(</sup><sup>2</sup>
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Pfreundschuh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 489; DB 2; L
Pred. No. 2.3e-48;
Pred. Mismatches 35;
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Tureci O, Sahin U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 175;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) 1 obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping proce
                                                                                                                                 spared
                                                                                                                                              Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury;
                                                                                                                                                                                             Human
                                                                                                                                                                                                                         29-JAN-2004
                                                                                                                                                                                                                                                                                    ADE56087 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 175
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                                                                       WO2003016475-A2
                                                                                                                                                                                                                                                         ADE56087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; SEQ ID NO 7967; 71pp + Sequence Listing; English.
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                                                                                                                                                                                           Protein P02511,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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                                                                                                                                   SNI;
                                                                                                                                                                                             SEQ ID NO 1928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 489; DB 3;
; Pred. No. 2.3e-48;
34; Mismatches 35
                                                                                                                                                                                                                                                                                       175
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171

59 55 6

14-AUG-2002; 2002WO-US025765

27-FEB-2003.

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RESULT 6
ADE75367
ID ADE7
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AC ADE7
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AC ADE7
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DT 29-J
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed medication but was obtained in alcottories.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a which is differentially regulated in an animal subjected to pain and a sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which is differentially regulated in an amount for identifying an agent kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of a first animal
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially
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                                             29-JAN-2004 (first entry)
                                                                                                                                   ADE75367 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that is differentially expressed in neuronal tissue of a first animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition comprising
                                                                                                                                                                                                                                                                                                                                60
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                                                                                                                                                                                                                                              VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH 115
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                                                                                                                                                                                                                                                                                       RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP--TSAP 171
                                                                                                                                                                                                                                                                                                                                WFDTGLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERODEHGFISREFH 119
                                                                                                                                                                                                                                                                                                                                                                                                                      MDIAIHHPWIRRPFFPFHSPSRLFDQFFGEHLLESDLFP-TSTSLSPFYLRPPSFLRAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQ--SLFR--T 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 but was obtained in electronic form directly from WIPO at
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                                                                                                                                 protein; 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      two or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 489; DB 7;
Pred. No. 2.3e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated polypeptides, useful for in an animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 175;
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Hybrid protein chaperone; protein stabilisation; heat shock protein; sHSP family, protein aggregation inhibition; cell death inhibition; genome stability pathway inhibition; protein denaturation identification; protein conformation related disease; cardiomyopathy; cataract; neurodegenerative disease; cardiant; ophthalmological; neuroprotective; gene therapy; alphaB-crystallin; human.
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Homo sapiens

WO2003091266-A2

06-NOV-2003.

23-APR-2003; 2003WO-GB001721.

23-APR-2002; 2002GB-00009334

(UYDU-) UNIV DUNDEE

Quinlan

WPI; 2003-865571/80

stabilizing proteins and/or protein activities, or as an agent to preve protein aggregation, or for treating diseases involving altered protein New hybrid protein chaperone (e.g. heat shock protein) useful for to prevent

Disclosure; Fig 11; 45pp; English

CC replacement of one or more regions of an sHSP with the corresponding CC region from a second sHSP can improve the activity compared to native SHSPs. In a particualr embodiment of the invention, the hybrid chaperone is a hybrid sHSP designated alphaB-HSP27 comprising the N-terminus and CC central portion of alphaB-crystallin and the C-terminal tail of HSP27. CC However, the hybrid protein chaperones of the invention can comprise regions from HSP90, HSP70 and HSP60 families as well as from the sHSP CC such as enzymes, therapuetic proteins, diagnostic proteins, reporter CC such as enzymes, therapuetic proteins, diagnostic proteins, reporter CC such as enzymes, therapuetic proteins, diagnostic proteins raducous conjugates in an aqueous conjugates in an aqueous conjugates in an aqueous comprising at least one protein chaperones; stabilised protein formulation chaperone; nucleic acids and vectors encoding a hybrid protein chaperone; conduction associated with the above hybrid protein chaperone; nucleic acids and vectors encoding a hybrid protein chaperone; con the coexpression of a recombinant protein of interest and a hybrid protein protein aggregation, as inhibitors of cell death and genome compromed the complex of the treatment of diseases involving altered comproment protein conformations (e.g., cardiomyopathies, cataracts or neurodegenerative diseases), or for the manufacture of a medicament for the treatment of such diseases. Sequences appr3533-ADB75373 represent primary sequence and chaperone properties: HSP90, HSP70, HSP60 and sHSP (small heat shock protein). The invention is based upon the finding that among the sHSP family, which have a general structure of a central domain (called the alpha-crystallin domain) flanked by N and C-terminal regions, proteins and/or protein activities. Protein chaperones (also known heat shock proteins) are divided into 4 families on the basis of the The invention relates to a hybrid protein chaperone for stabilising members of the sHSP family which may be used in hybrid protein The invention is based upon the finding that chaperones

Sequence 175 ĀĀ;

밁 Ś Matches Query Match ocal Similarity MDIAIHHPWIRRPFFPFHSPSRLFDQFFGEHLLESDLFP-TSTSLSPFYLRPPSFLRAPS MDVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQ--SLFR--T 55 Conservative 53.4%; Score 489; DB 7; 54.5%; Pred. No. 2.3e-48; 34; Mismatches 35; Length 175; Indels 12; Gaps 59

56 VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH 115

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Human sHSP family member, alphaB-crystallin

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RESULT 7
AAG03887
ID AAG03887
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XX AAG0
XX Huma
XX Huma
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XX EP1C

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                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; SEQ ID NO 7968; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC03893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy;
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                                                                                   56 VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted
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                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               250
RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP--TSAP 171
                                                                                                                                                                                                              MDVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQ--SLFR--T
                                                          WFDTGLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFH
                                                                                                                                                                      MDIAIHHPWIRRPFFPFHSPSRLFDQFFGEHLLESDLFP-TSTSLSPFYLRPPSFLRAPS
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                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 forensic, gene
                                                                                                                                                                                                                                                                                                                                                                                                               ΑA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein,
                                                                                                                                                                                                                                                                                                                      54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duclert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tag; secreted protein; cDNA isolation,
                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy and
                                                                                                                                                                                                                                                                                       Score 489; DB 3;
Pred. No. 3.9e-48;
4; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Þ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome mapping procedures.
                                                                                                                                                                                                                                                                                          35;
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RESULT 8
AAR87512
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                                                                                                                                                                                                                                                                                                                                                                                               CC This sequence represents human alpha B crystallin. This protein os CC located in the eye lens, and also in striated muscle, kidney and CNS CC tissue. Within the normal CNS, alpha B crystallin is mainly found in CC oligodendrocytes located in the white matter. It has been shown that CALPHA B crystallin is highly homologous to heat shock proteins and has CC been found to exhibit chaperone characteristics. Immunohistochemical CC studies have shown that cellular levels of alpha B crystallin increase as CC a result of stress. Also in a number of pathological conditions, e.g. CC alzheimer's and Alexander's disease, levels of alpha B crystallin are CC elevated. Immunohistochemical staining of CNS tissues with anti-alpha B CC crystallin antibodies revealed enhanced expression within or close by CC multiple sclerosis (MS) lesions as compared to unaffected regions of CC white matter. Alpha B crystallin is thought to be the autoantigen in MS compared to the autoantigen in MS cand is is the target of various modifications, e.g. phosphorylation. There are only four amino acid differences between bovine and human alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Best Local (
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of alpha B crystallin in diagnosis and treatment of auto:immune disease - esp. multiple sclerosis, also therapeutic use of specific antagonists, auto:reactive T cells or their T-cell receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; alpha B crystallin; eye lens; striated muscle; kidney; central nervous system; oligodendrocyte; white matter; heat shock protein; chaperone characteristic; stress; hlzheimer's disease; Alexander's disease; antibody; multiple s
                                                                                                                                                                                                                                                                                                                    Sequence 175
                                                                                                                                                                                                                                                                                                                                                                                  B crystallin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 3; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-040357/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR87512 standard;
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56 VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH 115
                                                                                                                                                                                          l Similarity
97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEDERLANDSE ORG TNO
                                                              MDIAIHHPWIRRPFFFFHSPSRLFDQFFGEHLLESDLFP-TSTSLSPFYLRPPSFLRAPS
                                                                                                        MDVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQ--SLFR--T
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                                                                                                                                                                                    Score 488; DB 2
Pred. No. 3e-48;
5; Mismatches
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                                                                                                                                                                                                                                               DB 2;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 168; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing or treating pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-543489/52.
N-PSDB; ACF25379.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUL-2001; 2001GB-00018354.
07-FEB-2002; 2002GB-00002883.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                           l Similarity
96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an isolated gene sequence in the screening of compounds
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                                                                                                                   WIDTGLSEMRMEKDRFSVNIDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFH 119
                                                                                                                                            VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH 115
                                                                                                                                                                                                                                       MDIAIHHPWIRRPEFPFHSPSRLFDQFFGEHLLESDLFS-TATSLSPFYLRPPSFLRAPS 59
                                  RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP--TSAP 171
                                                                                                                                                                                                                                                                                            MDVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQ--SLFR--T
RKYRIPADVDPLTITSSLSSDGVLTVNGPRKQ-
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dixon
                                                                                                                                                                                                                                                                                                                                                        52.9%; Score 485; DB 6; Length 175; 53.9%; Pred. No. 6.8e-48; ive 36; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       central sensitisation pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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-ASGPERTIPITREEKPAVTAAP 173
                                                                                                                                                                                                                                                                                                                                                              12;
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RESULT 10 ADB99861 ID ADB99

ADB99861

standard; protein; 175

Human skeletal muscle stress protein,

15-MAR-1996

(first entry)

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RESULT 11
AAR78692
ID AAR78
XX
AC AAR78
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DT 15-M2
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                       and which has nootropic, neuroprotective, antiparkinsonian and anticonvulsant activity. The compositions are specifically used to treat or prevent Alzhaimer's, Pick's, Huntington's and Parkinson's diseases and also for diagnosis. DNA sequences that encode alpha-1-antitrypsin (aaT), or its fragments, are useful for isolating homologous RNA or DNA sequences, and for recombinant production of aaT in gene therapy. This sequence represents the mouse alpha-B cristallin alpha (SWISS PROT No: P23927) used in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; antiparkinsonian; anticonvulsant; Alzheimer's Pick's disease; Huntington's disease; Parkinson's disease; alpha-1-antitrypsin; aaT; gene therapy; alpha-B cristallin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel composition for treatment or prevention of neurodegenerative disease containing at least one protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        especially alphal-antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for treating or preventing neurodegeneration, Alzheimer's or Parkinson's diseases, contains protease in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2001; 2001DE-01048553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-2002; 2002WO-EP010937.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disease; protease inhibitor; nootropic;
                                                                                          AAR78692 standard;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; SEQ ID NO 5; 40pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-371960/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meyer H, Klose J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse alpha-B cristallin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB99861;
                                                             AAR78692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROT-)
                                                                                                                                                                    120
                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                        56 VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGVISREFH 115
                                                                                                                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTAGEN AG
                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                    WIDTGLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFH
                                                                                                                                                                                                RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSA 170
                                                                                                                                                                                                                                                                                         MDIAIHHPWIRRPFFPFHSPSRLFDQFFGEHLLESDLFS-TATSLSPFYLRPPSFLRAPS
                                                                                                                                                                                                                                                                                                                     MDVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQ--SLFR--T 55
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                52.0%;
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                                                                                                                                                                                                                                                                                                                                                   Pred. No. 7.66
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Score 476; DB 7;
Pred. No. 7.6e-47;
                                                                                           AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease inhibitor,
                                                                                                                                                                                                                                                                                                                                                                                 Length 175;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                 119
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Best Local Similarity
                                          hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antitheumatic; antithyroid; antiviral; antibacterial; antifungal; antitheumatic; antithyroid; antivinamenic; gene therapy; cancer; proliferative disorder; hypottension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of a new human stress protein p20. The stress protein can be used as a diagnostic agent for autoimmune dise. Antibodies raised against the protein can be used in immunoassays to detect the presence of the protein and in a new protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New stress protein p20,
directed against it - us
auto:immune disease.
           allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 160 AA;
                                                                                                                                                                                                                                                                 08-FEB-2001
                                                                                                                                                                                                                                                                                                                            AAB42472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-285570/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p20; stress protein; muscle; diagnosis; autoimmune disease; dimer.
   thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPVAQVPTDPGHFSVLLDVKHFSPEEIAVKVVGEHVEVHARHEERPDEHGFVAREFHRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRY 118
                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                        RLPPGVDPAAVTSALSPEGVLSI-
                                                                                                                                                                                                                                                                                                                                                                                                                                      RLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPVQPSWLRRASAPLPGLSAPGRLFDQRFGEGLLEAELAALCPTTLAPYY---LRAPSVA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTIQHPWFKRTLGPF----YPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 2;
                                                                                                                                                                                                                                   ORF2236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93JP-00327666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9pp;
                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                  polypeptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.1%;
40.1%;

    its purification and synthesis,
useful as a diagnostic reagent in

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Japanese.
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                                                                                                                                                                                                                                                                                                                            160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 340; DB 2;
Pred. No. 4.8e-31;
1; Mismatches 50
                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                  SEQ ID NO:4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                                                                                                                                                        -QAAPASAQAPPPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 160
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the
              coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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detection
                                                                                                       hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                        158
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                                                                                                                                                                      cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The new disease.
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ABG93941
ID ABG
XX
AC ABG
XX

ABG93941 standard;

protein; 160

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Best Local
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05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                      cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antimugal; antirheumatic; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency storage, systemic lupus crythematosus, severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                           Sequence 160
                                                                                                                                                                                                                                                                                                                                               (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmund disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 3657; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999;
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                                                                                                                                                                                                                                                 Local
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                                                                            62 LPVAQVPTDPGHFSVLLDVKHFSPEEIAVKVVGEHVEVHARHEERPDEHGFVAREFHRRY
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                                                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                            VTIQHPWFKRTLGPF----YPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLD
                                      RLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSA
                                                                                                                SGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRY 118
RLPPGVDPAAVTSALSPEGVLSI--
                                                                                                                                                      VPVQPSWLRRASAPLPGLSAPGRLFDQRFGEGLLEAELAALCPTTLAPYY---LRAPSVA
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                             AA,
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                                                                                                                                                                                                                                                   37.1%;
                                                                                                                                                                                                                               Score 340; DB 3;
Pred. No. 4.8e-31;
%1; Mismatches 50
                                                                                                                                                                                                                                   50;
-QAAPASAQAPPPAA
                                                                                                                                                                                                                                                                       Length 160;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                   22;
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                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune
    158
                                                                                                                                                                                                                                 Gaps
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26-NOV-2002

(first entry)

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CC polypeptide, for stimulating mesenchymal cell growth and/or division by C exposing animal mesenchymal cells to conditioned media or its active CC fraction, obtained from deer antler cartilage cells, for inhibiting cell crowth and/or division by inserting into an animal cell, a compound which combine the translation of the polynucleotide encoding the DACC. The CC method and the polypeptides are useful for stimulating mesenchymal cell cc growth and/or division or for stimulating condrogenesis, cartilage, disc cor connective tissue growth, repair, regeneration and/or restoration in cc an animal. The polynucleotides, polypeptides, agonists and antagonists cm an animal in treatment modalities, specifically in gene therapy. The cc polypeptides can be used as bait proteins in a two- or three-hybrid assay considered in treatment modalities, specifically in gene therapy. The colypeptide and are involved in modulating cell growth and/or division. The sequences presented in ABG93923-ABG93948 are the proteins encoded by the DACC cDNA clones
                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to transfecting these cells and chondrocytes with vectors carrying the genes of these polypeptides capable of stimulating chondrogenesis, osteogenesis, growth, repair, repeareration and/or restoration of the extracellular matrix. The chondrocytes selectively express genes required to form a cartilaginous matrix. The DACC polypeptides and polynucleotides are useful for identifying an agent that modulates the activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention discloses a method for stimulating or inhibiting cell growth and/or division which comprises contacting or inserting into an animal cell a polypeptide comprising one of the deer antler cartilage cell (DACC) clones disclosed. More particularly, the method relates to these polypeptides stimulating mesenchymal cell growth and/or division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stimulating or inhibiting cell growth and/or division, useful for stimulating chondrogenesis, cartilage, disc or connective tissue growth, repair, and/or regeneration, comprises administering deer antler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; deer; rat; mouse; DACC; deer antler cartilage cell; cell stimulation; cell inhibition; cell growth; cell division; mesenchymal cell; chondrocyte; chondrogenesis; osteogenesis; growth; repair; regeneration; restoration; extracellular matrix; cartilaginous matrix; cartilage; disc; connective tissue; agonist;
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 136-137; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-2002; 2002WO-AU000163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antagonist; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide orthologous to DACC-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roubin R, Ghosh P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-2001; 2001AU-00003116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2002
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                                                                                                                                                                                                      Similarity
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                                          VTIQHPWFKRTLGPF----YPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLD
VPVQPSWLRRASAPLPGLSAPGRLFDQRFGEGLLEAELAALCPTTLAPYY---LRAPSVA 61
                                                                                                                                                                                                                                                                                                                            160 AA;
                                                                                                                                                                    Conservative
                                                                                                                                                                                                  37.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIT
                                                                                                                                                        31;
                                                                                                                                                            Score 340; DB 5;
Pred. No. 4.8e-31;
31; Mismatches 50
                                                                                                                                                                50;
                                                                                                                                                                                                                                        Length 160;
                                                                                                                                                                Indels
                                                                                                                                                            22;
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SGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRY 118

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VPVQPSWLRRASAPLPGLSAPGRLFDQRFGEGLLEAELAALCPTTLAPYY---LRAPSVA 61

VTIQHPWFKRTLGPF----YPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLD 58

37.1%; Score 340; DB 5; Length 160 40.1%; Pred. No. 4.8e-31; tive 31; Mismatches 50; Indels

22;

Gaps

Query Match Best Local S Matches 69

Similarity

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ABSULT 14
ABP43873
ID ABP43873
XX ABP43873
XX ABP43873
XX ABP438
XX Neuro
CYCOS
XW Cytos
XW Cytos
XW Cytos
XW WOUND
XX Homo
XX
                                                                                                                                                                                                                                                                                                     vulnerary, neuroprotective, immunomodulator, cytostatic and anti-
inflammatory. Compositions comprising nucleic acids of the invention are
useful for treating a mammalian subject, or as nutritional sources or
supplements. These are useful in gene therapy, particularly for treating
wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or inflammation.
Sequence 160
                                                                amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABP43544-ABP43989 represent polypeptides encoded by polynucleotides of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID # 776; 357pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABQ61117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2000; 2000US-00687527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; anti-inflammatory; gene therapy; nutritional suppleme wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human skeletal muscle stress protein p20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2001; 2001WO-US027760.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP43873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĄJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 LPVAQVPTDPGHFSVLLDVKHFSPEBIAVKVVGEHVEVHARHEERPDEHGFVARBFHRRY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| || :|:::|| :|:|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein;
       ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou P,
Wehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunomodulator; cancer; chromosome 19pter-q12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             undi V, Zhang
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----QAAPASAQAPPPAA 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         supplement;
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SGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRY 118

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RESULT 15
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             proteins or antibodies, their fragments or conjugates in an aqueous solution using hybrid protein chaperones; stabilised protein formulation comprising at least one protein associated with the above hybrid protein chaperone; nucleic acids and vectors encoding a hybrid protein chaperone, and the coexpression of a recombinant protein of interest and a hybrid protein chaperone. The hybrid protein chaperones are useful as agents to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hybrid protein chaperone (e.g. heat shock protein) useful for stabilizing proteins and/or protein activities, or as an agent to prevent protein aggregation, or for treating diseases involving altered protein
                                                                                                                                                                                    region from a second SHSP can improve the activity compared to native SHSPs. In a particual embodiment of the invention, the hybrid chaperon is a hybrid SHSP designated alphaB-HSP27 comprising the N-terminus and central portion of alphaB-crystallin and the C-terminal tail of HSP27. However, the hybrid protein chaperones of the invention can comprise regions from HSP90, HSP70 and HSP60 families as well as from the sHSP
                                                                                                                                                                                                                                                                                                                                         primary sequence and chaperone properties: HSP90, HSP70, HSP60 and sHSP (small heat shock protein). The invention is based upon the finding that among the sHSP family, which have a general structure of a central domain (called the alpha-crystallin domain) flanked by N and C-terminal regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid protein chaperone; protein stabilisation; heat shock protein; sHSP family; protein aggregation inhibition; cell death inhibition; genome stability pathway inhibition; protein denaturation identification; protein conformation related disease; cardiomyopathy; cataract; neurodegenerative disease; cardiant; ophthalmological; neuroprotective;
                                                                                                                                                such as enzymes,
                                                                                                                                                                                                                                                                                                                                                                                                                               proteins and/or protein activities. Protein chaperones (also known as heat shock proteins) are divided into 4 families on the basis of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a hybrid protein chaperone for stabilising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 11; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conformations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-865571/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002; 2002GB-00009334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2003; 2003WO-GB001721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; HSP20; human.
                                                                                                                                                                                                                                                                                                                     replacement of one or more regions of an sHSP with the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human sHSP family member, HSP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE75368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE75368 standard; protein; 160 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIV
                                                                                                                The invention also encompasses methods for stabilising proteins enzymes, therapuetic proteins, diagnostic proteins, reporter or antibodies, their fragments or conjugates in an account protein their fragments or conjugates in an account protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLPPGVDPAAVTSALSPEGVLSI-----
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                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                         protein conformations (e.g., cardiomyopathies, cataracts or neurodegenerative disease), or for the manufacture of a medicament for the treatment of such diseases. Sequences ADE75363-ADE75373 represent
                                                                                                                                                                                                                                                                                        Sequence 160 AA;
                                                                                                                                                                                                                                                                                                                                       members of the sHSP family which may be used in hybrid protein chaperones
                                                                                                                                                                                                                                                                                                                                                                                                              stability pathways, for identification of proteins that are in the process of unfolding, for the treatment of diseases involving alter
                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                           the invention.
 122
                                 119
                                                                   62 LPVAQVPTDPGHFSVLLDVKHFSPEBIAVKVVGEHVEVHARHEERPDEHGFVAREFHRRY
                                                                                                        59
                                                                                                                                                                                                                 69;
                                                                                                                                          σı
                                                                                                                                                                           3 VTIQHPWFKRTLGPF----YPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLD
                                                                                                                                                                                                                                  Similarity
RLPPGVDPAAVTSALSPEGVLSI--
                                 RLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSA 170
                                                                                                    SGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRY
                                                                                                                                          VPVQPSWLRRASAPLPGLSAPGRLFDQRFGEGLLEAELAALCPTTLAPYY---LRAPSVA
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                              37.1%;
                                                                                                                                                                                                             ; Score 340; DB 7;
; Pred. No. 4.8e-31;
31; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                              diseases involving altered
                                                                                                                                                                                                               50;
QAAPASAQAPPPAA
                                                                                                                                                                                                                                                 Length 160;
                                                                                                                                                                                                               Indels
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 158
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Search completed: September 27, 2004, 13:20:16
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution.
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"Vertebrate lens alpha-crystallins are
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Weleber R.G.;
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Litt M., Kramer P., la Morticella D.M., Murphey W.,
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Biochemistry 39:15791-15798(2000)
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                                                                                                                                                                                                                                     PTM: O-glycosylated; contains N-acetylglucosamine side chains.

PTM: IN LENS, MOST DEAMIDATION OF ASN-101 OCCURS DURING THE FIRST 30 YEARS OF AGE, FOLLOWED BY A SMALL ADDITIONAL AMOUNT OF DEAMIDATION (APPROXIMATELY 5%) DURING THE NEXT APPROXIMATELY 38 YEARS, RESULTING IN A MAXIMUM OF APPROXIMATELY 50% DEAMIDATION DURING THE LIFETIME OF THE INDIVIDUAL.

DISEASE: Defects in CRYAR are the cause of zonular central nuclear cataract [MIM:123580]. It is one of a considerable number of phenotypically and genotypically distinct forms of autosomal dominant cataract [MIM:604219]. This congenital cataract is a common major abnormality of the eye that frequently cause blindness in infants.
                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EMEUropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                  family.
                                                                                                                                                                                                                      SIMILARITY: Belongs to the small heat shock protein
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CARBOHYD
VARIANT
               de Jong W.W., van der Ouderaa F.J., Versteeg
van Amelsvoort J.M., Bloemendal H.;
"Primary structures of the alpha-crystallin I
                                                                                                                            NCBI
                                                                                                                                                                                                                                 Alpha crystallin CRYAA.
                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01,
01-OCT-1996 (Rel. 34,
30-MAY-2000 (Rel. 39,
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P02488;
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Vision.
                                                                                                                                            Cercopithecinae;
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SWISS-2DPAGE; P02489; HUMAN
                                                                                SEQUENCE
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THA -> HT (IN REF. 2
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O-LINKED (GLCNAC) (BY SIMILARITY).
R -> C (in zonular central nuclear
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Pred. No. 6.1e-82;
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CONFLICT
              Alpha crystallin CRYAA.
                                                                                     CRAA_LOXAF
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InterPro; IPR003090; Crystallin_N.
InterPro; IPR002068; Hsp20.
InterPro; IPR0030978; HSP20_chap.
Pfam; PF00525; crystallin; 1.
Pfam; PF00011; HSP20; 1.
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Biochemistry 35:3578-3586(1996).
-!- FUNCTION: May contribute to the transparency and refractive
                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A02890;
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between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the lens.
-!- SIMILARITY: Belongs to the small heat shock protein
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Unpublished results, cited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96241614;
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  loxodonta
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Jaworski C.J.;
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PD001193; Crystallin_N; 1.
; PS01031; HSP20; 1.
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1 1 ACETYLATION (POBABLE)
168 168 O-LINKED (GLCNAC).
153 154 TH -> HT (IN REF. 1).
172 AA; 19792 MW; 1F7AF9066BEEB2D7 CRC
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96139023; PubMed=8587135;
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A reassessment of mammalian alpha A-crystallin sequences using sequencing: implications for anthropoid affinities of tarsier.";

Sequencing: implications for anthropoid affinities of tarsier.";

ONL. Evol. 41:901-908 (1995).

-I- FUNCTION: May contribute to the transparency and refractive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0299; ACRYSTALLIN.

PRODGE; PRO01193; Crystallin N; 1.

PROSTIE; PS01031; HSP20; 1.

Eye lens protein; Acetylation; Glycoprotein.

MOD RES
1 1 ACTYLATION.

CARBOHYD 162 162 O-LINKED (GLCNA
SEQUENCE 173 AA; 19837 MW; E6DESCD8C838F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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InterPro; IPR008978; HSP20_
Pfam; PF00525; crystallin;
Pfam; PF00011; HSP20; 1.
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Mammalia; Eutheria;
NCBI_TaxID=9785;
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95.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 884; DB 1;
Pred. No. 7.8e-79;
6; Mismatches 2
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Vstallin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC)
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chains
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3 CRC64;
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rictions on its
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RESULT 5
CRAA_CAVPO
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Best Local
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CONFLICT
                                                                                                                                                                                                                                                                                                                           Eye lens
MOD RES
MOD RES
                                                                                                                                                                                                                                                                                                                                                                    ProDom; F
PROSITE;
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Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE=93151974; PubMed=8427639;
Parveen R., Smith J.B., Sun Y., Smith D.L.;
"Primary structure of rabbit lens alpha-crystallins.";
J. Protein Chem. 12:93-101(1993).
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSp20_chap.
Pfam; PF00525; crystallin; 1.
Pfam; PF00011; HSP20; 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             de Jong W.W., van der Ouderaa F.J., Versteeg M., Groenewoud G. van Amelsvoort J.M., Bloemendal H.; "Primary structures of the alpha-crystallin A chains of seven mammalian species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL
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Mammalia; Butheria;
CRAA_CAVPO
                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001436; Crystallin_alpha.
InterPro; IPR003090; Crystallin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A02896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X95382; CAA64668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family.
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                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                PR00299; ACRYSTALLIN.
                                                                                                                                                                                                     MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
                                                                                 PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
                                                                                                                                         ISBVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVBIHGKHNERQDDHGYISREFHRRYRL
                                                                                                                                                                            MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                     PSNVDQSALSCSLSADGMLTFSGPKVQSGLDAGHSERAIPVSREEKPSSVPSS
                                                                                                                        ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQEDFVEIHGKHNERQDDHGYISREFHRRYRL
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162
170
173 i
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                                                                                                                                                                                                                                                                                     AA;
 STANDARD;
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162
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                                                                                                                                                                                                                                             96.0%;
95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quinl A.N., Redd A.N., Russell S., the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                      WW;
                                                                                                                                                                                                                                Score 879; DB 1;
Pred. No. 2.4e-78;
5; Mismatches 3;
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V -> A (IN REF. 2)
; C12C25298CC327EA
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 PRT;
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  173
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  A
                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
                                                                                                                                                                                                                                                          Length 173;
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tions on its
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PIR; E94432; CYCPAA.

InterPro; IPR001436; Crystallin_al
InterPro; IPR003090; Crystallin_N.
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_chap.
Pfam; PF00525; Crystallin; 1.
Pfam; PF00011; HSP20; 1.
                                                                                                                                                                                                                                               CRÁA EULFU STANDARI

P02494;

21-UUL-1986 (Rel. 01, 02)

21-UUL-1986 (Rel. 01, 12)

15-UUL-1999 (Rel. 38, 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 0
21-JUL-1986 (Rel. 0
15-JUL-1999 (Rel. 3
Alpha crystallin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0299; ACRYSTALLIN.

PRODOR; PD001193; Crystallin N; 1.

PROSITE; PS01031; HSP20; 1.

Eye lens protein; Acetylation; Glycoprotein.

MOD RES 1 1 1 ACETYLATION (PROBABLE).

MOD RES 1 1 1 ACETYLATION (PROBABLE).

CARBOHYD 162 0-LINKED (GLYCAR)

CARBOHYD 162 0-LINKED (GLYCAR)
de Jong W.W., Zweers A.,
"Trends in the molecular
(In) Peeters H. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protides of the biological fluids, Proc. Pergamon Press, Oxford (1980).
-!- FUNCTION: May contribute to the tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de Jong W.W., Zweers A., Goodman M.;
"Trends in the molecular evolution of alpha-crystallin.";
(In) Peeters H. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pedetes capensis (Springhaas).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                             Alpha crystallin A
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                                                                 PARTIAL SEQUENCE.
                                                                                                               NCBI_TaxID=40322;
                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                         Eukaryota; Metazoa;
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173 AA;
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                                                                                                                                                                                                                                                                                                                                          STANDARD;
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38,
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19807 MW;
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                                                                                                                                       Chordata;
Primates;
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Crystallin_N.
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95.4%;
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Last annotation updat
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Pred. No. 3e-78;
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                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Strepsirhini; Lemuridae; Eulemur.
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Best Local S
Matches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OCHPR
                 Pfam; PF00525; crystallin; 1.
Pfam; PF00011; HSP20; 1.
PRINTS; PR00299; ACRYSTALLIN.
ProDom; PD001193; Crystallin N;
PROSITE; PS01031; HSP20; 1.
                                                                                                             InterPro; IPR001436; Crysta
InterPro; IPR003090; Crysta
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_
                                                                                                                                                                                                                                                                                                                                             de Jong W.W., Zweers A., "Trends in the molecular
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Lagomorpha; Ochotonidae: Ochoton
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21-JUL-1986 (Rel. 01, Last
15-JUL-1999 (Rel. 38, Last
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MOD RES
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                         Protides of the biological fluids, Proc. Pergamon Press, Oxford (1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha crystallin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P02492;
                                                                                                                                                                                             PIR; A02895; CYOIAA.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9978;
                                                                                                                                                                                                                                                                                                                               (In) Peeters H.
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                                                                                                                                                                                                                             of the lens.
SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                   FUNCTION: May
                                                                                                                                                                                                             family.
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SIMILARITY: Belongs
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Pro; IPR003090; Crystallin_N.
Pro; IPR002068; Hsp20.
Pro; IPR008978; Hsp20_chap.
Pr00525; crystallin; 1.
PF00011; Hsp20; 1.
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 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
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1 1 ACETYLATION (PI
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Acetylation; Glycoprotein.
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94.8%;
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LCNAC) (BY SIMILARITY).
BB5ED37 CRC64;
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for

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entities requires a license agreement (som send an email to license@isb-sib.ch).

Pfam; PF00525; crystallin; Pfam; PF00011; HSP20; 1.

PD001193;

Crystallin_N; 1.

PR00299; ACRYSTALLIN

InterPro; IPR001436; Crystallin_alpha.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; Hsp20_chap.

PIR; A02898; CYLPAA. EMBL; U24068; AAA97570.1;

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RESULT
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Best Local S
Matches 164
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de Jong W.W. Zweers A., Goodman M.
"Trends in the molecular evolution of
(In) Peeters H. (eds.);
Protides of the biological fluids,
Pergamon Press, Oxford (1980).
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between
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                 "A reassessment of mammalian alpha A-crystallin sequences using sequencing: implications for anthropoid affinities of tarsier."

J. Mol. Evol. 41:901-908(1995)
                                                                                                                                                                                                                                                                                                                                    MEDLINE=96139023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perodicticus potto edwarsi (Potto), and Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus). Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Perodicticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-UIL-1986 (Rel. 01, Created)
21-UIL-1986 (Rel. 01, Last sequence up
15-UIL-1999 (Rel. 38, Last annotation
Alpha crystallin A chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERPO
                                                                                                                                                                                                                                                                                                                           Jaworski C.J.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 121-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL
                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a comment the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is by non-bis statement is not removed. Usage by and for ities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                     family.
                                                                                                                                                                                                                                              of the lens.
SIMILARITY: Belongs to
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173 AA;
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162
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Pred. No. 9.2e-78;
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O-LINKED (GLCNAC) (BY SIM
, 77B8CAFB749A3A5C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             of alpha-crystallin.";
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Best Local
                                                                                                                                                                                                                   Matches 162;
                                                                                                                                                                                                                                                                              Query Match
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MOD_RES
CARBOHYD
SEQUENCE
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21-JUL-1986
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eye lens
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CRYAA.

Procavia capensis (Cape hyrax) (Rock uasses, Procavia capensis (Cape hyrax) (Rock uasses, Procaviata; Vertebrata; Rukaryota; Metazoa; Chordata; Procavidae; Procaviata; Procaviatae; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001436; Crystallin_alpha.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR002068; Hsp20.
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_chap.
Pfam; PF00525; Crystallin; 1.
Pfam; PF00011; HSP20; 1.
PFINTS; PR002299; ACRYSTALLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=77158093; PubMed=870070;
de Jong W.W., Nuy-Terwindt E.C., Versteeg M.;
"Primary structures of alpha-crystallin A chains of elephant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
15-JUL-1999 (Rel. 38,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hyrax and rhinoceros.";
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SIMILARITY: Belongs
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; PS01031; HSP20; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSEVRSDRDKFVIFLDVKHFSPEDLTVKVQEDFVEIHGKHNERQDDHGYISREFHRRYRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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| ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL
                                                                                                                                 MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
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                                                                                                 MDVTIQHPWFKRALGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
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173 AA;
                                                                                                                                                                                                                                                                                                                                             173 AA;
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                                                                                                                                                                                                                      Conservative
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1 ACETYLATION (PROBABLE).
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19805 MW;
                                                                                                                                                                                                                                                                                                                                             19822 MW;
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                                                                                                                                                                                                                      8,
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ACETYLATION (PROBABLE)
O-LINKED (GLCNAC) (BY
; 33B1C8079BB5ED37 CRC
                                                                                                                                                                                                                                                  Score 873;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                          O-LINKED (GLCNAC) (BY SIMILARITY).
T -> A (IN 50% OF THE MOLECULES).
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.2e-78;
                                                                                                                                                                                                                                                     DB 1;
.2e-78;
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                                                                                                                                                                                                                                                                                        Procavia
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RESULT CRANKER REPORT R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat),
Meriones unguiculatus (Mongolian jird)
Mesooricetus auratus (Golden hamster),
Tupaia glis (Tree shrew)
                                                                                                                                                                                                                                           MEDLINE=93054670; PubMed=1429679; Srinivasan A.N., Nagineni C.N., Bhat S.P.; "Alpha A-crystallin is expressed in non-oc J. Biol. Chem. 267:23337-23341(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moormann R.J.M., van der Velden H.M.W.,
Bloemendal H., Schoenmakers J.G.G.,
"An unusually long non-coding region in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de Jong W.W., van der Ouderaa F.J., Versteeg
van Amelsvoort J.M., Bloemendal H.;
"Primary structures of the alpha-crystallin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The alternative splicing product alpha Ains structurally equivalent to alpha A and alpha alpha crystallin aggregate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=Rat; STRAIN=Sprague-Dawley; Bhat S.P., Nandy P., Srinivasan A., Cheng D., Submitted (JAN-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; Sturer TaxID=10090, 10116, 10047,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha crystallin A chain, CRYAA OR CRYA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                  protein-coding inform Cell 32:707-712(1983)
                                                                         King C.R., Piatigorsky J.; "Alternative RNA splicing of the murine alpha A-crystallin protein-coding information within an intron.";
                                                                                                                                             SEQUENCE FROM N.A.
SPECIES=Mouse;
MEDLINE=83155647; PubMed=6187470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Biochem. [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammalian species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   de Jong W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=Rat;
MEDLINE=90105511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090,
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21-JUL-1986 (Rel. 01, C
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     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   SPECIES=Rat
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 90-172 FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                         messenger RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 53-173 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=82081811; PubMed=6171772;
                                                                                                                                                                                                                                                                                                                                                                                                                     Acids Res. 9:4813-4822(1981).
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     OF 11-173 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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ink H., Voorter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acta 1037:58-65(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus 0116, 10047, 10036, 9395;
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alpha B subunits
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J databases.
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SALA LA PARTA PART
     Query Match
Best Local S
Matches 164
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R InterPro; IPR001345; Crystallin_N.

R InterPro; IPR003090; Crystallin_N.

R InterPro; IPR003090; Crystallin_N.

R InterPro; IPR002068; HSP20 chap.

Pfam; PF00525; Crystallin; 1.

R Pfam; PF0051; HSP20; 1.

R Pfam; PF00011; HSP20; 1.

R PRINTS; PR00299; ACRYSTALLIN.

R PRODOm; PD001193; Crystallin_N; 1.

PROSON; PS01031; HSP20; 1.

R PROSON; PS01031; HSP20; 1.

R PROSON; PS01031; HSP20; 1.

ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U47922; AAA93367.1; --
EMBL; V01219; CAA24530.1; --
EMBL; M96949; AAA40644.1; --
EMBL; M96950; AAA40645.1; --
EMBL; J00376; AAA37471.1; --
EMBL; J00375; AAA37469.1; --
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EMBL; J00375; AAA37468
PIR; A02892; CYRTA.
PIR; A02893; CYMSA.
PIR; C94432; CYHYAB.
PIR; D94432; CYHYAB.
                                                                                                                        CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=M.unguiculatus, and M.auratus; de Jong W.W., Zweers A., Goodman M.; "Trends in the molecular evolution of alpha-crystallin."; (In) Peeters H. (eds.); Protides of the biological fluids, Proc. 28th colloquium, Pergamon Press, Oxford (1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlycoSuiteDB; P02490; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Jong W.W., Zweers A., Versteeg M., Nuy-Terwindt E. "Primary structures of the alpha-crystallin A chains mammalian species, chicken and frog.";
Eur. J. Biochem. 141:131-140(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=T glis; TISSUE=Lens; MEDLINE=84208008; PubMed=6723655; de Jong W.W., Zweers A., Versteeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-33119896; PubMed=7156978;
King C.R., Shinohara T., Piatigorsky
"Alpha A-crystallin messenger RNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
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     thes 164;
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ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collable een the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
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                           Similarity
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173
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124
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                         95.1%;
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gs to the smal
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Score 871; DB 1;
Pred. No. 1.4e-77;
5; Mismatches 4
                                                                                                                     ACETYLATION.
O-LINKED (GLCNAC)
V -> M (IN REF. 5
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small heat shock protein
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                                               Length 173;
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21-JUL-1986 (Rel. 01, 0
21-JUL-1986 (Rel. 01, 1
15-JUL-1999 (Rel. 38, 1
Alpha crystallin A cha:
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InterPro; IPR003090; Crystallin
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSp20_chap.
                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: May contribute to the transparency and refractive of the lens.
-!- SIMILARITY: Belongs to the small heat shock protein (HSP20)
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de Jong W.W., Zweers A., Goodman M.;

"Trends in the molecular evolution of alpha-crystallin.";

[In) Peeters H. (eds.);
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Mammalia; Eutheria; Chiroptera;
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
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                                                                          PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
                                                                                                              ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL
                                                                                                                                            MDITIQHPWFKRALGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
                                                      PSNVDQSALSCSLSADGMLTFSGPKLQSGVDGGHSERAIPVSREEKPSSAPSS
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93.6%;
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No. 2.3e-77;
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Query Match
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21-JUL-1986
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                                                                                                                                                    InterPro; IPR001436; Crystallin alpha.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_chap.
Pfam; PP00525; Crystallin; 1.
Pfam; PP00011; HSP20; 1.
                                                                                                                                                                                                                                                                                   the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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CRYAA OR CRYA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roquemore E.P., Dell A., Morris H.R., Panico M., Reason A.J., Savoy L.-A., Wistow G.J., Zigler J.S. Jr., Earles B.J., Hart G.W.; "Vertebrate lens alpha-crystallins are modified by O-linked N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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8
8
                                                                                                                                                                                                                                 PIR; A29656; CYBOA.
GlycoSuiteDB; P02470; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         acetylglucosamine.";
T Biol. Chem. 267:555-563 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith J.B., Thevenon-Emeric G., Simth I "Elucidation of the primary structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=74075721; PubMed=4770792; van der Ouderaa F.J., de Jong W.W., Bloe
"The amino-acid sequence of the alphaA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of a bovine lens alpha A-crystallin Biochem. Biophys. Res. Commun. 148:31-37(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88049675; PubM
Hay R.E., Petrash J.M.
                                       SEQUENCE
                                                                                                     Eye
                                                                                                                                                                                                                                                            EMBL; M26142; AAA30471.1;
                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYDRATE-LINKAGE SITE SER-162.
MEDLINE=92112709; PubMed=1730617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91253722; PubMed=2042736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, ACETYLATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-crystallin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                  PROSITE;
                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                            sioi. Chem. 267:555-563(17)
FUNCTION: May contribute
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs
                                                                                                                                                                                                                                                                                                                                                                                                                    of the lens.
                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. 193:118-124(1991).
                                                                                                                                PD001193;
                                                                                                                                            PR00299; ACRYSTALLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                   protein;
                                                                                                                  PS01031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Bovine).
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(Rel.
(Rel.
                                     173
                                                               \frac{122}{162}
                                     AA;
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01, Last
38, Last
A chain.
                                                                                                                 Crystallin_N; 1. HSP20; 1.
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                                                                                                      Acetylation; Phosphorylation;
                                                                122
162
                                        19790
94.9%;
94.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                         to
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                                    O-LINKED (GLCNAC).
/FTId=CAR_000056.
; 7796ED1B71864478
  Score 869;
Pred. No. 2
                                                                             PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                to the transparency and refractive
                                                                                           ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                         small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simth D.L.,
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chain of bovine
  DB 1;
.3e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green
                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                   Glycoprotein
             Length
                                        CRC64;
              . 173;
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RESULT 13
CRAA_TAPIN
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                                                                                                                                                          Matches 162;
                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                       MOD
                                                                                                                                                                                                                                                                                                   InterPro; IPR001436; Crystallin_alpha.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR002068; Hsp20.
InterPro; IPR002068; Hsp20 chap.
InterPro; IPR008978; HSp20 chap.
Pfam; PF00525; crystallin; 1.
Pfam; PF00011; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (In) Peeters H. (eds.);
Protides of the biological fluids, Proc.
Pergamon Press, Oxford (1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammaalia; Eutheria; Perissodactyla; Tapiridae; Tapirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha crystallin CRYAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P02476;
21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRAA
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                    PIR; A02878; CYTPAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tapirus indicus (Asiatic tapir) (Malayan tapir).
                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Trends in the molecular evolution
                                                                                                                                                                                                            lens protein; Acetylation; Glycoprotein.
RES 1 1 ACETYLATION (PROBABLE).
BOHYD 162 162 O-LINKED (GLCNAC) (BY SIM
UENCE 173 AA; 19804 MW; 7629BD05806942DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   family.
                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the small heat shock protein (HSP20)
                                                                                                                                                                                                                                                                                                                                                                                                                          of the lens.
                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: May contribute to the transparency and refractive index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
                                                                                                                                                                                                                                                              PD001193; Crystallin_N; 1. ; PS01031; HSP20; 1.
                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                        PR00299; ACRYSTALLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDIAIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDVTIQHEWEXRTLGPEYPSRLEDQFFGEGLFEYDLLPELSSTISPYYRQSLERTVLDSG
                                                                 ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL
                                                                                                                               MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSNVDQSALSCSLSADGMLTFSGPKIPSGVDAGHSERAIPVSREEKPSSAPSS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQEDFVEIHGKHNERQDDHGYISREFHRRYRL
PŚŃVDQTALSCSIŚADGMITFSGPKVPSGLDAGHSERAIPVSREEKPSSAPSS
                       PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
                                                                                                       MDIAIQHEWEKRTLGEEYPSRLEDQEEGGEEYDLLEELSSTISEYYRQSLERTVLDSG
                                                   ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQEDFVEIHGKHNERQDDHGYISREFHRRYRL
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                                                                                                                                                                    94.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodman M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                     Score 868; DB 1;
Pred. No. 2.8e-77;
                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of alpha-crystallin.";
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CRAA_BALAC

RESULT 14

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RESULT 15
CRAA GIRCA
ID "CRAA G
AC P02471
DT 21-JUL
DT 15-JUL
DT 15-JUL
DE Alpha
GN CRYAA.
OS Giraff
OS Hippop
OC Eukary
OC Mammal
OC Giraff
OX NCBI 1
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RP PARTIA
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Best Local S
Matches 161
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Pfam; PF0U52.,
Pfam; PF0U011; HSP2U,
Pfam; PF0U011; HSP2U,
PRINTS; PR00299; ACRYSTALIN.,
PRINTS; PR001193; Crystallin N; 1.
PRODOM; PD001193; HSP2U; 1.
R PROSITE; PS010131; HSP2U; 1.
R PROSITE; PS010131; HSP2U; 1.
1 1 ACETYLATION (PROBABLE).
PSY Length 173;
162 O-LINKED (GLCNAC) (BY SIMILARITY).
DA9AZBD25B1959DF CRC64;
O:
                                                                                                                                                                                                                                                          CRAA GIRCA
P02471;
21-JUL-1986
21-JUL-1986
15-JUL-1999
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P02474;

21-JUL-1986 (Rel. C

21-JUL-1986 (Rel. C

15-JUL-1999 (Rel. C

15-JUL-1999 (Rel. C

Alpha crystallin A

CRYAA.
  PARTIAL :
                                                               Giraffa camelopardalis (Giraffe), and Hippopotamus amphibius (Hippopotamus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoi Giraffidae; Giraffa. MCBI_TaxID=9894, 9833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=77158093; PubMed=870070; de Jong W.W., Nuy-Terwindt E.C., Verstee "Primary structures of alpha-crystallin hyrax and rhinoceros.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                                                                  21-JUL-1986 (Rel. (
21-JUL-1986 (Rel. (
15-JUL-1999 (Rel. :
15-JUL-1999 (Rel. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003090; Crysta
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 491:573-580(1977)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Balaenopteridae;
NCBI_TaxID=9767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the small heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the lens.
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  SEQUENCE.
W.W., Zweers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSNVDQSALSCSLSADGMLTFSGPKVPSGMDAGHSERAIPVSREEKPSSAPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQEDFVEIHGKHNERQDDHGYISREFHRRYRL
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                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                       A chain.
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. 01, Last sequence 38, Last annotations.
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PIR; A94432; CYGPAA.

InterPro; IRR001436; Crystallin_alpha.

InterPro; IPR003099; Crystallin_N.

InterPro; IPR002068; Hsp20.

InterPro; IPR002068; Hsp20.

InterPro; IPR008978; HSP20.chap.

Pfam; PF00525; Crystallin; 1.

Pfam; PF00011; HSP20; 1.
                                                                                                                                                                                                   Eye lens protein; Acetylation; Glycoprotein.

MOD RES 1 1 ACETYLATION (PROBABLE).

CARBOHYD 162 162 0-LINKED (GLCNAC) (BY SIM

SEQUENCE 173 AA; 19760 MW; DB312BCCAAF659CE CRC64;
                                                                                                                                                                                                                                                   PRINTS; PR00299; ACRYSTALLIN.; ProDom; PD001193; Crystallin_N; PR05101E; PS01031; HSP20; 1.
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ides of the biological fluids,
impon Press, Oxford (1980).
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PSNVDQSALSCSLSADGMLTFSGPKIPSGVDAGHSERAIPVSREEKPSSAPSS
              PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
                                                               ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL
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Search completed: September 27, 2004, 13:20:31 Job time: 12 secs

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Q9dev0 clarias fus
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Q9pf3 spalax yuda
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Q9pur2 brachydanio
Q9deu9 clarias fus
Q804e0 clarias fus
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ALIGNMENTS

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61 ISEVRSDRDKFVIFLDVKHESPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL 120		1 MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYROSLFRTVLDSG 60	Matches 135; Conservative 22; Mismatches 16; Indels 0; Gaps 0;	Match 82.9%;	SEQUENCE 173 AA; 19951 MW; D7DBCBDDCC87B858 CRC64;	ProDom; PD001193; Crystallin_N; 1.	PIAM; PROUDIL; HSP2O; 1. PRINTS; PROUZ99; ACRYSTALLIN.		InterPro; IPR008978; HSP20 chap.	InterPro; IPR002068; Hsp20.	InterPro; IPR003090; Crystallin N.	Interpro. IDRO11436 Crystallin alsha	ENGI. DAGAGA DAGAGAI 1.		in embryonic and	Mizuno N., Agata K., Sawada K., Mochii M., Eguchi G.;	SEQUENCE FROM N.A.	[1]	NCBI TaxTD=R310:	Chordata;	Cynops pyrrhogaster (Japanese common newt).	A-crystallin.	(TrEMBLrel. 25, Last	(TrEMBLrel. 21,	01-JUN-2002 (TremBLrel. 21, Created)		OSOFUS PRELIMINARY: PRT: 173 ha	ff 1

Q9gn07 bombyx mori Q13684 homo sapien O18634 plodia inte Q95p25 ciona intes Q96c20 homo sapien

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                                                                                                                                                            Q8UUZ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99251119; PubMed=10234811; Mizuno N., Mochii M., Takahashi T.C., "Lens regeneration in Xenopus is not a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha A crystallin.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W6T3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9W6T3
                                     Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii; T
Cyprinidae; Danio
                                                                                                       01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Alpha A crystallin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D88185; BAA76897.1; -. InterPro; IPR001436; Crystallin_alpha. InterPro; IPR003990; Crystallin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         development, with respect to crys Differentiation 64:143-149(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002068; Hsp20.
InterPro; IPR008978; Hsp20 chap.
Pfam; PF00525; crystallin; 1.
Pfam; PF00011; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
                         NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00299; ACRYSTALLIN.
PD001193; Crystallin_N; 1.
; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
                                                                                                                                                                                                                                                                                                                                                  PASVDQSSITCSLSTDGMLTFSGTKMQSSLDSSHGERPIPVSREEKPASAQSS 173
                                                                                                                                                                                                                                            ISEVRSDRDKFVIFLDVKHESPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL 120
                                                                                                                                                                                                                                                                                                                                                                           MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFBYDLLFFLSSTISFYYRQSLFRTVLDSG
                                                                                                                                                                                                                                                                      PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSA 170
                                                                                                                                                                                                                                                                                                  ISEVRSDRDRFVINLDVKHFSPEDLSVKVHDDFVEIHGKHNERQDDHGYISREFHRRYRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 AA;
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19789 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       80.3%; Score 736; DB 13;
77.1%; Pred. No. 8.9e-67;
tive 26; Mismatches 13;
                                                                                                                      20,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to crystallin
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Last annotation update)
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                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                  Created)
                                                      ) (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             96190D9FC5B7E712 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ы
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mere repeat of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression.";
                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Best Local S
Matches 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Chiou S.-H., Yu C.-M.;

T Alpha crystallin of catfish eye lenes: cDNA and genomic ana Talpha-B.";

T Alpha-A and Alpha-B.";

EMBL; AY007972; AAG23866.1; -.

R EMBL; AY007972; AAG23866.1; -.

R InterPro; IPR0001436; Crystallin alpha.

R InterPro; IPR003090; Crystallin_N.

R InterPro; IPR003090; Crystallin_N.

R InterPro; IPR002068; Hsp20.

R InterPro; IPR008978; HSP20.

R InterPro; IPR008978; HSP20.

R Pfam; PF00525; crystallin; 1.

R Pfam; PF00511; HSP20; 1.
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ZFIN; ZDB-GENE-020508-1; Crystallin_alpha.
InterPro; IPR001436; Crystallin_N.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR002068; Hsp20.
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_chap.
Pfam; PF00525; crystallin; 1.
Pfam; PF00011; HSP20; 1.
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PRINTS; PRO0299; ACRYSTALLIN.
PRODOm; PD001193; CLYStallin N; 1.
PROSITE; PS01031; HSP20; 1.
SEQUENCE 173 AA; 19714 MW; 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Runkle S., Hill J., Kantorow M., "Cloning and characterization of crystallin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinopterygii; Neopterygii; Teleostei; Clariade; Clarias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-A crystallin.
Clarias fuscus (Whitespotted clarias)
Eukaryota, Metazoa, Chordata, Craniat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                               PRINTS; PR00299; ACRYSTALLIN.; 1.
PRODOM; PD001193; Crystallin.; 1.
PROSTTE; PS01001; HSP20; 1.
SEQUENCE 173 AA; 19705 MW; 93A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9DEV0;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9DEV0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=33541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
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                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS
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                                         MDVTIQHPWFKRTLGDFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLD--
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MDIAIQYPWFRRTLS--NPSRLFDQFFGEGLLDHDLLPFTASTISPSYRHSLFRSFLDSS
                                                                                                                                                   71.3%;
ilarity 70.5%;
Conservative 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.8%; Score 694; DB 13; 72.2%; Pred. No. 1.7e-62;
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                                                                                                                                                           23;
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Last sequence up
Last annotation
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24; Mismatches
                                                                                                                                                           Score 653; DB 13;
Pred. No. 2.5e-58;
3; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301D743DB91BBC13 CRC64;
                                                                                                                                                                                                                                                                                                                       93ABEDAB122C9724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ostariophysi; Siluriformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
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on update)
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                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 173;
                                                                                                                                                                                                                                     Length 173;
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            58
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subterranean mole-

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RESULT
Q99NDZ
ID Q9
D7
O11
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Q9EPF3
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Best Local :
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InterPro; IPR008978; HSP20_chap.
Pfam; PF00525; Crystallin; 1.
Pfam; PF000011; HSP20; 1.
PR.NTS; PR00299; ACRYSTALLIN.
PRODOm; PD001193; Crystallin N; 1.
PROSITE; PS01031; HSP20; 1.
                                                                                                                                             Q9EPF3;
Q9EPF3;
01-MAR-2001
01-MAR-2001
01-OCT-2003
                                                                                         01-OCT-2003 (TrEMBLrel.
Alpha-B-crystallin.
ALPHA-B-CRYSTALLIN.
                                  Spalax judaei.
Bukaryota; Met
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The evolutionary fate of mole rat alpha-A-crystallin: indispensable eye lens protein?";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases EMBL; AJ272441; CAC33095.1;
InterPro; IPR001436; Crystallin alpha. InterPro; IPR003090; Crystallin N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spalax leucodon ehrenbergi (El
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nannospalax.
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                 RKYRIPADVDPLTITSSLSSDGVLTVNGPRKQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIDTGLSEMRMEKORFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDIAIHHPWIRRPFFFHSPSRLFDQFFGEHLLESDLFS-TSTSLSPFYLRPPSFFRAPS
           l; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
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170 AA;
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                                                                                                                                                                                                    (TrEMBLrel.
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                                                                                                                                                                                                                                                              PRELIMINARY;
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        Chordata;
Rodentia;
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ta; Craniata; Vertebrat
ia; Sciurognathi; Murid
                                                                                                                                             Last
Last
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Pred. No. 1.5e-41
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        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                           PRT;
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annotation
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thi; Muridae; Spalacinae;
                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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     Euteleostomi;
; Spalacinae;
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                                                                                   AID DACE OCCORD DE COMMENTA DE
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  Best
                            Query Match
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InterPro; IPR001436; Crystallin alpha.
InterPro; IPR003090; Crystallin N.
InterPro; IPR003090; Crystallin N.
InterPro; IPR008081; HSp20.
InterPro; IPR008978; HSP20_chap.
Pfam; PF000525; Crystallin; 1.
Pfam; PF000511; HSP20; 1.
PRINTS; PR00299; ACRYSTALLIN.
PRODOm; PD001193; Crystallin N; 1.
PROSTTE; PS01031; HSP20; 1.
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01-JUN-2003
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                                                                                   SEQUENCE
                                                                                                           PRINTS; PR00299; ACRYSTALLIN.
PRODOM; PD001193; Crystallin N;
PROSITE; PS01031; HSP20; 1.
NON_TER 1
                                                                                                                                                                                                  Pfam; PF00525; Lize-Pfam; PF00011; HSP20; ACRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92111524; PubMed=1765091;
Bhat S.P., Horwitz J., Srinivasan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Anza population; TISSUE=Heart, ar MEDLINE=21142392; PubMed=11245977; Avivi A., Joel A., Nevo E.; "The lens protein alpha-B-crystallin of rat: high homology with sighted mammals. Gene 264:45-49(2001).

EMBL; Au293658; CAC01692.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                 InterPro; IPR001436; Crystallin_alpha.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20 chap.
InterPro; IPR008978; HSP20 chap.
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S77142; AAP31996.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Alpha B-crysi
in the lens."
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STRAIN=Anza popula
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NCBI_TaxID=134510;
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  Local
                                                                                                                                                                                                                                          PF00525; crystallin;
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97; Conserv
  Similarity
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                                                                                   176
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                 ĀΑ;
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Rodentia;
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52.4%;
53.7%;
                                                                                 20168 MW;
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54.5%; Pred. No. 1.5e-41;
tive 35; Mismatches 34
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Score 480;
Pred. No.
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Sciurognathi; Muridae;
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independent
0; DB 11;
. 9.9e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae;
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Q9PUR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning, sequencing and differential expression of in the zebrafish, danio rerio(1)."; Biochim. Biophys. Acta 1447:271-277(1999).

EMBL; AF159089; AAD49056.1; -.

ZFIN; ZDB-GENE-991119-2; cryab.
InterPro; IPR001436; Crystallin_alpha.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR008089; HSP20.
InterPro; IPR0080978; HSP20.
InterPro; IPR0080978; HSP20.
Pfam; PF00525; crystallin; 1.
Pfam; PF005119; Crystallin, 1.
PFDDOm; PF001193; Crystallin_N; 1.
PROSITE; PS01031; HSP20; 1.
Q9DEU9;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9PUR2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha b crystallin.
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                                                              Q9DEU9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20011287; PubMed=10542326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHR 116
                                                                                                                                                                                                                                                                                                                                                                                  MDVTIQHPWFKRTLGP-FYPSRLFDQFFGBGLFEYDLLFFLSSTISPYYRQSLFRTVL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYRIPADVDPLTITSSLSSDGVLTVNGPRKO----ASGPERTIPITREEKPAVTAAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDTGLSEMRMEKORFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFHR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIAIHHPWIRRPFFPFHSPSRLFDQFFGEHLLESDLFS-TATSLSPFYLRPPSFLRAPSW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQ--SLFR--TV
                                                                                                                                                                                                                                                                                    ----DSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISR 112
                                                                                                                                                                                                                                                              FPSWWDSGMSEMRQDRDRFVINLDVKHFSPDELTVKVNEDFIEIHGKHDERQDDHGIVAR
                                                                                                                                                                           EFFRKYKIPAGVDPGAITSSLSSDGVLTINTLRHQLDI---
                                                                                                                                                                                                                 EFHRRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP 167
                                                                                                                                                                                                                                                                                                                                                MEISIQHPWYRRPLFPGFFPYRIFDQYFGEHLSDSD--PF----SPFYTMFYYRPYLWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kantorow M., Horwitz J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
  (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   50.1%; Score 458.5; DB 13; 52.0%; Pred. No. 1.4e-38; tive 33; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
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Last annotation updat
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  Last sequence update)
                        Created)
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Q804E
D0 Q804E
AC Q804E
AC Q804E
AC Q804E
DT 01-UU
DT 01-OC
DE Alpha
OS Clari
OC Actir
OC Actir
OC Clari
OC III
DC III
DC III
DC III
DC III
DC III
DR FAMM
DR Pfam
DR PFAMS
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Best Local
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Alpha-B crystallin.
Clarias fuscus (Whitespotted clarias).
Eukaryota; Metazoa; Chordata; Cramiata;
Actinopterygii; Neopterygii; Teleostei;
Claridae; Clarias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00525; crystallin; 1.

Pfam; PF00011; HSP20; 1.

PRINTS; PR00299; ACRYSTALLIN.

ProDom; PD001193; Crystallin_N; 1.

PROSITE; PS01031; HSP20; 1.

SEQUENCE 172 AA; 19831 MW; 74D
                             PRINTS; PRO0299; ACRYSTALLIN.
PRODOM; PD001193; Crystallin N; 1.
PROSITE; PS01031; HSP20; 1.
SEQUENCE 172 AA; 19831 MW; 74D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q804E0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q804E0
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                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=59899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
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SEQUENCE FROM N.A.

Chiou S.-H., Yu C.-M., Chao Y.-K.;

Chipha-A and alpha-B.";

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ dat EMBL; AX184812; AA024775.1; -

Chember of IPR00301436; Crystallin alpha.

InterPro; IPR003090; Crystallin alpha.

InterPro; IPR003090; Crystallin Alpha.

InterPro; IPR003089; Hsp20.

InterPro; IPR00308978; Hsp20.

Pfam; PF00525; Crystallin; 1.

Pfam; PF00525; Crystallin; 1.

Pfam; PF00511; Hsp20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ol-JUN-2003 (TrEMBLrel. 24, Created)
ol-JUN-2003 (TrEMBLrel. 24, Last sequence
ol-CCT-2003 (TrEMBLrel. 25, Last annotatio
Alpha-B crystallin.
Clarias batrachus (walking catfish).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii, Neopterygii; Teleostei; Os
Clariidae; Clarias.
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InterPro; IPR001436; Crystallin_Alpha.
InterPro; IPR003090; Crystallin_N.
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_chap.
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Chiou S.-H., Yu C.-M., Chao Y.-K.;
Chiou S.-H., Yu C.-M., Chao Y.-K.;
"Alpha crystallin of catfish eye lenes: cDNA and genomic alpha-A and alpha-B.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRR 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESGLSEMKMEKDRFTINLDVKHFTPEELGVKVSGDYIEVHAKHEDRQDDHGFVSREFHRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRVPSGVDFTSITSSLSSDGVLTITAPRKPS--DA--PERSITITREDKSVGSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.2%; Score 441.5; DB 1
49.1%; Pred. No. 7.9e-37;
                                                                                                                                                                                                                                                                                                                                                                                                 catfish eye lenses: cDNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74DC93030396AB64 CRC64;
74DC93030396AB64 CRC64;
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Ostariophysi;
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                                                                                                                                                                                                                                                                                                                                                databases
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RESULT 11
09359
AC 09359
AC 09359
AC 09359
DT 01-NO
DT 01-OC
DE Alpha
OS Astya
OC Charar
OC Charar
OC CASTI
RN [1] -
RP SEQUE
RC STRAI
RX MEDLI
RX MEDLI
RX MEDLI
RX Hehre
RT struc
RI epige
RT struc
RI Gene
DR Inter
DR FEAM;
DR PFAM;
DR PFAM;
DR PFAM;
DR PFAM;
DR PROSIC
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Best Local S
Matches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002068; Hsp20.
InterPro; IPR008978; Hsp20_chap.
Pfam; PF00525; crystallin; 1.
Pfam; PF00011; Hsp20; 1.
PRINTS; PR00299; ACRYSTALLIN.
PRODom; PD001193; Crystallin_N; 1.
PROSITE; PS01031; Hsp20; 1.
PROSITE; PS01031; Hsp20; 1.
SEQUENCE 208 AA; 22568 MW; D32AE
                                        Q9GN07;
01-MAR-2001
01-MAR-2001
           Heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Astyanax fasciatus (Blind cave fish) (Astyanax mexicanus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Characiformes;
Characidae; Astyanax.
                           01-OCT-2003
                                                                                         Q9GN07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behrens M., Wilkens H., Schmale H., "Cloning of the alphaA-crystallin genes of a blind cave form epigean form of Astyanax fasciatus: a comparative analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-epigean fish; TISSUE-Spleen; MEDLINE-98398454; PubMed-9729440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TremBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    093592;
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001436; Crystallin_alpha.
InterPro; IPR003090; Crystallin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 216:319-326(1998).
EMBL; Y11300; CAA72158.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-A-crystallin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structure, expression and evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                              . Similarity 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ш
                                                                                                                                                                                                                                               MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLD---
                                                                                                                                                                  NSGMSEVRSDRDKFMVYLDVKHFSPEELNVKVAEDYVEIQGKHGERQ
                                                                                                                                                                                                                             MDIATOHPWFRRALG--YPSRLFDQFFGEGLFDYDLFPYATSTVSPYYRYSLFRNFLDSS
                                                                                                                                                                                           -SGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YRVPSGVDPTSITSSLSSDGVLTITAPRKPS--DA--PERSITITREDKSVGSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WDVTIQHPWFKRTL-GPFYPSRLFDQFFGEGLEEYDLLPFLSSTISPYYRQSLFR--TVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGLSEMKMEKDRFTINLDVKHFTPEELGVKVSGDYIEVHAKHEDRQDDHGFVSREFHRK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDIAIQHPWFRRSFWQSFFPSRIFDQHFGEHVSESEVLAPYPSVYCP--RPSFFRWPSWV
         1 (TrEMBLrel. 16, 0
1 (TrEMBLrel. 16, 1
3 (TrEMBLrel. 25, 1
protein hsp20.8A.
             protein
                                                                                                                                                                                                                                                                                              Conservative
                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.2%;
49.1%;
                                                                                                                                                                                                                                                                                       46.2%; Score 423.5; DB 13; 72.9%; Pred. No. 6.8e-35; 72.9%; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                          Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation updat
                           Last annotation
                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 441.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                        D32AE17C07244D83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                          sequence
                                                                                         186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208
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                                        update)
                                                                                                                                                                                                                                                                                                                          DB 13; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
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RESULT 13
Q13684
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       Query Match
Best Local S
Matches 55
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Best Local S
Matches 64
                                                                                                                                               PROSITE;
NON_TER
NON_TER
SEQUENCE
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Q13684;
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"Jeolation, identification and particular expression of shock genes in silkworm, Bombyx mori.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF315319; AAG30946.1;

EMBL; AF315317; AAG30946.1;

InterPro; IPR001435; Crystallin_alpha.

InterPro; IPR002068; Hsp20.

InterPro; IPR002068; Hsp20.

InterPro; IPR002068; Hsp20.
                                                                                                                                                                                                                                                                                   InterPro; IPR001436; Crystallin_alpha.
InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_chap.
Pfam; PF00011; HSP20; 1.
PRINTS; PR00299; ACRYSTALLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-CCT-2003 (TrEMBLrel. 25, Last annotation
nlpha-A-crystallin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Exp. Eye Res. 59:125-126(1994).
EMBL; L25781; AAC37570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=95137069; PubMed=7835394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00011; HSP20; 1.
PRINTS; PR00299; ACRYSTALLIN.
PROSITE; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caspers G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 CSLSADGMLTFCGPKIQTGLDATHAERAIPVSR
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           55;
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                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                     PS01031; HSP20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPSRLVDQDFGLALTPNDMLAAVACPVLS---EDYFRPWRQLAAASRDLG-SSIKADKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRLSSDGVLTITAPRKVP--DAVKGERKVPIAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPSRLFDQFFGEGLFEYDLL----PFLSSTISPYYR--QSLFRTVLDSGISEVRSDRDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQVNLDVQHFSPEEISVKTADGYIVVEGKHEEKKDEHGYISRQFVRRYALPEGAAPETVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequence corrects
                                                                                                                                                  95
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                       56
                                                                                                                                                  ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pennings
                                                                                                                                                  6121 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                        32.0%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.2%; Score 294.5; DB 5 41.8%; Pred. No. 7.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Jong W.W.;
       0;
Score 293; DB 4;
Pred. No. 2.4e-22;
D; Mismatches 1
                                                                                                                                                  4898A44D349EA0F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F8956B919BF978CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human alpha A-crystallin primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                     Length
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  small heat-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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   Gaps
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Q95P2
ID Q95P2
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DT 01-DE
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DE Heat
OS Ciona
OC Eukar
OC Eukar
OC Phleb
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RN [1]
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RR [T]
RN [1]
RR TISSU
RR MEDLI
RA WENDA
RI GENES
DR EMBLI,
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Best Local
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O1-JAN-1998 (TrEMBLrel. 05, Creat
O1-JAN-1998 (TrEMBLrel. 05, Last
O1-OCT-2003 (TrEMBLrel. 25, Last
Alpha-crystallin cognate protein
                                                                                                                                                                                                                                                                                                                                                                   Q95P25;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Heat shock protein HSP27-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plodia interpunctella (Indianmeal moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
Pyralidae; Phycitinae; Plodia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    018634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0299; ACRYSTALLIN.
PROSITE; PS01031; HSP20; 1.
SEQUENCE 185 AA; 20639 MW; AA492D095535C44C CRC64;
                          SEQUENCE FROM N.A.
TISSUE-Body wall muscle;
TISSUE-Body Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tissue-Tis
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Shirk P.D., Broza R., Hemphill M., Perera O.P.;
"alpha-Crystallin protein cognates in eggs of the moth, Plodia
interpunctella: possible chaperones for the follicular epithelium yolk
                                                                                                                                                                                                                                                 NCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q95P25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insect Biochem. Mol. Biol. 28:151-161(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPSNVDQSALSCSLSADGMLTFCGP-KIQTGLDATHAERAIPVSR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-SNIKADKDKLQINLDVQHFSPEEISVKTADGFVVVEGKHEEKKDEHGYISRQFVRRYA
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  IPR001436; Crystallin_alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.0%; Score 293; DB 5; ilarity 41.2%; Pred. No. 1.1e-21; Conservative 25; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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InterPro; IPR008978; HsP20_chap.
Pfam; PF00011; HSP20; 1.
PRINTS; PR00299; ACRYSTALLIN.
PROSITE; PS01031; HSP20; 1.
SEQUENCE 190 AA; 21416 MW; 131826BF7B591550 CRC64;
126 HEKEDDHGVVSRDFTRKYTIPPNVDPLTVTSSLSPDGILTVEAPIRAIQAPTSLSVQHLE 185
                            101
                                                         66
                                                                                                                     17 YERSWOTFYDMPTSSLEDODFGSAPMSADFDLA--
                                                                                                                                                10 FKRTLGPFY---PSRLFDQFFGEGLF--EYDLLPFLSSTISPYYRQSLFR------
                                                                                                                                                                                66;
                                                                                                                                                                                            Similarity
                       NERQDDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFCGP----KIQTGLDATHAE 156
                                                     TAGVPIVPRAPMYTROLSGGMSQVTTDENKFKVTLDVKHFTPEBITVKTVDGAIEVHGKH
                                                                                                                                                                                Conservative
                                                                                ----TVLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKH 100
                                                                                                                                                                                            31.7%;
                                                                                                                                                                              26; Mismatches
                                                                                                                                                                                            Score 290; DB 5;
Pred. No. 2.3e-21;
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Search completed: September Job time: 42 secs 27, 2004, 13:21:18

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Database
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                 299
289.5
288
283
283
197
171.5
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
      389414 seqs, 51625971 residues
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916
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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                             US-09-107-532A-4324
US-09-252-991A-28807
US-09-489-039A-10634
US-09-489-039A-10685
US-09-489-039A-10
US-08-473-750-7
US-08-4773-750-7
US-08-4773-750-7
US-08-4773-735
US-09-252-991A-23899
US-08-480-917-2
US-08-480-917-2
US-08-480-917-2
US-09-118-736-2
US-09-118-736-2
US-09-118-7318-3
US-09-118-7318-3
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US-09-913-783A-170

US-09-900-407-4

US-08-900-407-4

US-09-553-498-6

US-09-618-86-9-6

US-09-618-86-9-6

US-09-621-976-7032

US-08-900-407-1
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(without alignments)
279.103 Million cell updates/sec
                        sequence 1, Appli
sequence 28807, A
sequence 10634, A
sequence 10685, A
sequence 10, Appl
sequence 10, Appli
sequence 1, Appli
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6, Appli
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7032, Ap
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US-08-900-407-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 3, Application US/08900407; Patent No. 5962262; GENERAL IMPORMATION: APPLICANT: Hillman, Jennifer
Best Local Similarity
            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman APPLICANT: Lal, I APPLICANT: Corley APPLICANT: Shah,
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Result No.

ALIGNMENTS

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; LIBRARY: Gen;
; CLONE: 63522
US-08-900-407-3
                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/900
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                             TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                         STRANDEDNESS:
                                                                                                                                       LENGTH: 193 amino acids
TYPE: amino acid
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CITY: Palo Alto
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Corley, Neil C.
Shah, Purvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
                                                                                                                           single
32.6%;
42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEW HUMAN HEAT SHOCK 27 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                DOS
                                                                                                                                                                                                                                                                                                                                                                               US/08/900,407
                                                                                                                                                                                                                                                       PF-0351
Score 299; DB 2;
Pred. No. 6.9e-28;
                                                                                                                                                                                                                                                       SD
                Length 193;
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                                                                                                                                                                                                                                                                                                        RESULT 3
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                                                                         GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW HUMAN HEAT SH
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
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SOFTWARE: PatentIn Ve
SEQ ID NO 170
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                                                                                                                                                                                                                                       Sequence 4, Application US/08900407 Patent No. 5962262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A Sys
FILE REFERENCE: 97-022-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/513,783A CURRENT FILING DATE: 2000-02-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 Match 31.6%; Score 289.5; DB 4; Local Similarity 37.9%; Pred. No. 3.4e-26; Les 77; Conservative 24; Mismatches 51;
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 RKYTLPPGVEATAVRSSLSPDGMLTVEAPLPKPAIQS--SEITIPVTVEAK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 PAAIESPAVAAPAYSRALSRQ-LSSGVSEIRHTADRWRVSLDVNHFAPDELTVKTKDGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH 115
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Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YHGSRLFDOSFGMPHIPEDWYKWPSGSAWPGYFR--LLPSESALLPAPGSPYGRA---LS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKRTLGP-----FYP-SRLEDOFFGEGLFEYDLLPFL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSLLRGPSWDPFRDWYPHSRLFDQAFG---
                                                                                                                                                                                                                                                                                                                                                                   -EITIPVTFESRAQLGGPEAAKS 453
                                                                                                                                                                                                                                                                                                                                                                                                       AERAIPVSREEK----PTSAPS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIHGKHNERODDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATH 154
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                                                                                                                        SHOCK 27 LIKE
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              ; SEQ ID NO 6
; LENGTH: 232
; TYPE: PRT
                                                                                                                                                                                                                                                                        Sequence 6, Application US/09553498
Patent No. 6309861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                         APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: Process for the production of naturally folded
FILE REFERENCE: Case 20379
CURRENT APPLICATION NUMBER: US/09/553,498
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: EP99107412.1
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                          APPLICANT: Schaeffner, Joer APPLICANT: Schaeffner, Joer APPLICANT: Schwarz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                      APPLICANT: Ambrosius, Dorothee APPLICANT: Rudolph, Rainer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,407
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TELECOMMUNICATION INFORMATION:
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CLONE: 662841
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REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                  178
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                                                                                                                                                                                                                                                                                                                                                                                -EITIPVTFESR 188
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RESULT 6
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; ORGANISM: Escherichia coli
US-09-618-869-6
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US-09-618-869-6
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SEQ ID NO 6
LENGTH: 232
Sequence 7032, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09618869 Patent No. 6455279
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schaeffner, Joerg
APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED
TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
TITLE OF INVENTION: CHAPERONES
FILE REFERENCE: 20381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/618,869
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR FILING DATE: 1999-07-29
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APPLICANT:
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30.9%; Score 283; DB 4;
Local Similarity 40.1%; Pred. No. 7.7e-26;
hes 75; Conservative 21; Mismatches 43
                                                                                                                                                                                 153
                                                                                                            209
                                                                                                                                            160 PVSREEK 166
                                                                                                                                                                                                           102 ERODDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFCG--PKIQTGLDATHAERAI 159
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                                                                                                                                                                                                                                                  94 TLAAPAFSRALNRQ-LSSGVSEIRQTADRWRVSLDVNHFAPEELTVKTKEGVVEITGKHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Ver. 2.1
                                                                                                          PVTFEAR 215
                                                                                                                                                                             ERQDEHGYISRCFTRKYTLPPGVDPTLVSSSLSPEGTLTVEAPLPKAVT----QSAEITI
                                                                                                                                                                                                                                                                                  STISPYYRQSLFRTVLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHN 101
                                                                                                                                                                                                                                                                                                                       PFRDWYPAHSRIFDQAFGVPRLPDEWSQWFSAAGWPGYVRPLPAATAEG-----PAAV
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                                                                                                                                                                                                                                                                                                                                                                                           30.9%; Score 283; DB 4; Length 232; 40.1%; Pred. No. 7.7e-26; ative 21; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
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NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 7032
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-7032
US-08-900-407-1
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Best Local
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                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/900,407 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Dr.
MMEDILL
LIBRARY: ::.
TONE: 1362715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NEW HUMAN HEAT SHOCK 27 LIKE TITLE OF INVENTION: PROTEIN
                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
                                                                 TOPOLOGY:
                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                               ENGTH:
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                                                                                                                 196 amino acids
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Lal, Preeti
                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
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                                                                               single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.5%; Score 197; DB 4; Length 60; 61.1%; Pred. No. 2.4e-16;
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                                                                                                                                                                                                                                36,749
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                                                        Best Local Similarity
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  DLLPFLSSTISPYYRQSLFRTVLDSGIS-----EVRSDRDKFVIFLDVKHFSPEDLTVKV 89
                                      10.5%; Score 96; DB 4; Length 139; 25.0%; Pred. No. 0.0012; ative 25; Mismatches 46; Indels
                                          22;
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US-09-107-532A-4324
                                                                            US-09-107-532A-4324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4324, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 4324:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: US/09/107,532A
                                                                                                NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...139
SEQUENCE DESCRIPTION: SEQ ID NO: 4324:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                FEATURE:
                                                                                                                                                                                                        HYPOTHETICAL: YE ORIGINAL SOURCE:
                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                   LENGTH: 139 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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US-09-252-991A-28807
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                                                                      US-09-489-039A-10634
                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 10634, Application US/09489039A ; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: ACID ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 28807
LENGTH: 154
TYPE: PRT
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                                                                                                                                                           SEQ ID NO 10634
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Query Match
Best Local Similarity
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PRIOR EILING DATE: 1998-02-18
PRIOR PRIOR EILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
                                                                                         ORGANISM: Klebsiella pneumoniae
                                                                                                              LENGTH: 191
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 10.0%; Score 92; DB 4; Length 154; Local Similarity 24.6%; Pred. No. 0.0041; es 34; Conservative 22; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 CGPK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 VLPK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 SNVDQSALSCSLSADGML 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 SDNTLTISANHESHTEDKEDGNYVRKERHSVSYKRSFYLP-NVDEEKITGTEK-NGVLKL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 QDDFVEI---HGKHNERQDDHGYISREFH-----RRYRLPSNVDQSALSCSLSADGMLTF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: | : || : |
11 DMFPDFNDVFSPAFNDFL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 DDEYRIVIAAAGFQEEDLDLQVERGVLTVSGGKREKSTDNVTYLHQGIAQRAFKLSFRLA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 RDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDH-----GYISREFHRRYRLP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 PLFRHSVG-----FDRF--NDLFESALRNEAGSTYPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 PWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSGISEVRSD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHIEVKAASL---ANGLL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09252991A
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    10.0%;
    Score 92;
Pred. No.
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       ; DB 4;
. 0.0056;
                         Length 191;
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RESULT 12
US-08-459-953A-10
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10685
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US-09-489-039A-10685
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                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08459953A Patent No. 6030822
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 10685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10685,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Lechne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 169
                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                          APPLICANT:
                                                                                                                       CORRESPONDENCE ADDRESS:
                                             STREET: Suite 4700
CITY: Los Angeles
                        COUNTRY:
                                          STATE:
                                                                      STREET: 633 West Fifth
STREET: Suite 4700
                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                           129 LSCSLSADGMLTFCGPKIQTGLDATHAERAIP--VSREEKP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
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        90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQVFTRFLEGENSMRNYDLSPLLRQWIGFDKLASALQTAGESQSFPPYNIEKSDDNHYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLALAGFRQEDLDIQLEGTRLVVKGTPQQPEKETTWLHQGLVSQAFSLSFTLADNMEVSG 134
                                      California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGMLTFCGPKIQTGLDATHAERAIPVSREEK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPEDLTVKVQDDFVEIHGKHNERQDDHGYI----SREFHRRYRLPSNVDQSALSCSLSA 135
                                                                                                                                                                                                                                        Lechner, Cornelia Moller, Niels P.H.
                      U.S.A
                                                                                                                                                                                                                    Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                      Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09489039A
                                                                                                                                                                                                                                                                                                                                                                                           ----ATFTNGLLHIDLTRNEPEQIAPQRIAISERP 165
                                                                                                                                                     EXTRACELLULAR SIGNAL-RELATED KINASE, SEQUENCES, AND METHODS OF PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 76.5; DB 22.4%; Pred. No. 0.35; tive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14342
                                                                                      Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
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US-09-393-212-10
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Matches
                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/09393212 Patent No. 6579972 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: March 19, 1
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 8.3%; Score 76; DB 3; Local Similarity 27.8%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                          COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                APPLICANT: Lechner, Cornelia
Moller, Niels P.H.
Ullrich, Axel
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: EXTRACELLULAR SIGNAL-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249
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               COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEMLTGRMLFAGAHELEQMQLILE----TIPVIREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGDFGLARIVDQHYSHK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETDLARLLEQGTLAEEHAKLEMYQLLRGLKYIHSAN---VLHRDLKPANIFISTEDLVLK 194
 SOFTWARE:
                                                                                                                                   STATE: California
                                                                                                                                                  CITY: Los Angeles
                                                                                                                                                                                   STREET: 633 West Fifth
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                                                                                                                                                                   Suite 4700
Microsoft Word
                                             storage
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                                                                                                                                                                                                                                                    KINASE,
METHODS
AND USE
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               IBM P.C.
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               DOS 5.0
                                                                 1.44 Mb
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Gaps

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US-08-277-231A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Sequence and Analysis of LKP Pilin Patent No. 5643725
TITLE OF INVENTION: Structural Genes and The LKP Pili (TITLE OF INVENTION: Haemophilus Influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08277231A Patent No. 5643725
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Green, Bi
APPLICANT: Brinton,
                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 44; Conserv
                                            FILING DATE: 19
CLASSIFICATION:
                                                            APPLICATION NUMBER: US/08/277,231A FILING DATE: 19-JUL-1994
                                                                                                                                                                                                                                                ZIP: 02173
                                                                                                                                                                                                                                                                                                                    CITY: Lexington
                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,212
FILING DATE: 09-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AEMLTGRMLFAGAHELEQMQLILE----TIPVIREE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 S--ADGMLTFCG----PKIQTGLDATHAERAIPVSREE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 IGDFGLARIVDQHYSHK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETDLARLLEQGTLAEEHAKLFMYQLLRGLKYIHSAN---VLHRDLKPANIFISTEDLVLK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EYDLLPFLSSTISPYYRQSLFRTVLDSGISEVRSDRDKFVIFLDVK----HFSPEDLTVK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQD----DFVEIHGKHNERQDDHGYISR----EFHRRYRL---PSN----VDQSALSCSL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/029,494 FILING DATE: March 19, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/459,953A
FILING DATE: June 2, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
Carroll, Alice O.
                                                                                                                                                                                                                                                                                               Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 586 amino acids
                                                                                                                                                                                                                                                                                                                                         Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.3%; Score 76; DB 4; Length 586; ilarity 27.8%; Pred. No. 2.5; Conservative 18; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Green, Bruce A.
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                                                                                                                                                                                                                                                                                                                                                              Hamilton, Brook,
                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                             Structural Genes and The IKP Pili Operon of No. 5643725typable Haemophilus Influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charles C.
                                                                                                                                                                                                                                                                                                                                                                Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GYLSEGLVTKWYRSPRILLSPNNYTKAIDMWAAGCIL 248
                                                                                                                                         Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US, Patent No. 5834187
Patent No. 5834187 5786143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5834187
Patent No. 5834187 5786143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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APPLICANT: Green, Bruce A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                      APPLICATION NUMBER: US 08/277,321
FILING DATE: 19-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC94-02B
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,542
REFERENCE/DOCKET NUMBER: ACT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/473,750
FILLING DATE: 07-UW-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Structural Gene and the LKP Pili Operon of No. 5834187 5786143t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Brinton, Jr., Charles C. TITLE OF INVENTION: Sequence and Analysis of LKP Pilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                          TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 FRQFSGAYLPEIYRPKNQFQVSLSQSLGNWGNLYLSG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 PLKHVSKNGYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 SRTFDERVLQGVLQYGLTNHLTLNSSLLYTRHYRAGLFGFGLNTPIGAFSADATWSHAEF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SRLFDQFFGEGLFEYDLLPFL----SSTISPYYRQSLFRTVLDSGISEVRSDRDKFVIFL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 DVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHG-----YISREFH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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Similarity 24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08473750
                                                                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               741 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (617) 861-9540
                                       617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jr., Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LPSNVDQSALSCSISADGMLTFCG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC94-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LHGSYSINFNESGTNITLAAYRYSSRDFYTLSDTIGLNRT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 76; DB 1; Length 741; Pred. No. 3.5;
                                                                                                 ACC94-02B
                                                                                                                                                                                                                                                                                                           Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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Search o Job time	D dd	Qy dd	Qy Db	Query Ma Best Loc Matches	; ; ; WS-08-4
Search completed: September 27, 2004, 13:22:17 Job time : 33 secs	118 YRLPSNVDQSALSCSLSADGMLTFCG 143	76 DVKHFSDEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHR 117	20 SRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSGISEVRSDRDKFVIFL 75 : : : :	Query Match 8.3%; Score 76; DB 2; Length 741; Best Local Similarity 24.2%; Pred. No. 3.5; Matches 38; Conservative 20; Mismatches 57; Indels 42; Gaps 5;	; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-473-750-7

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Result
No.
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Maximum DB s
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Maximum Match 100%
Listing first 45 summaries
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849.5
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_PUB.pep:*
        100.0
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92.7
74.6
69.8
58.0
54.5
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53.4
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916
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       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
 US-10-657-740-1
US-10-316-253-113
US-10-657-740-10
US-10-657-740-12
US-10-657-740-12
US-10-657-740-13
US-10-657-740-18
US-10-657-740-18
US-10-657-740-11
US-10-657-740-11
US-10-657-740-11
US-10-408-765A-405
US-10-226-956-297
US-10-226-956-299
US-10-226-956-299
US-10-229-386-27955
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                                                                                                                                                                                                                                                                              Description
Sequence 1, Appli
Sequence 113, App
Sequence 10, Appli
Sequence 11, App
Sequence 2, Appli
Sequence 3, Appli
Sequence 18, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 104, App
Sequence 297, App
Sequence 297, App
Sequence 299, App
Sequence 299, App
Sequence 299, App
Sequence 299, App
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4. 4. 4. 17	3	42	41	40		38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
66 00T	101	101.5	103	105	106.5		٠	115	147	150	150	154.5	188.5	188.5	266	277.5	283	284.5	288	288	288.5	ന	289.5	ന	289.5	m	336	338
10.8		11.1		•	•	11.7	2	12.6	16.0	٠	6.	٠,	20.6		9.			31.1	۲	۲	31.5	۲.	۲	۲	۲	۲	٥	36.9
153	161	208	195	160	207	153	245	159	186	145	145	145	143	143	136	205	209	102	471	199	205	459	205	205	205	0	S	160
12	12	15	12	12	16	14	15	15	16	15	15	16	15	15	16	16	16	12	10	16	14	14	16	15	14	12	16	14
US-10-424-599-176081 US-10-424-599-161149	-10-424-599-16	-10-310-154-6	0-424-599-24669	0-424-599-1466	0-767-701-4	98-	4-047-	-10-104-047-3	-10-408-765A-20	-10-369-493-642	0-369-493-	-10-657-740-7	-10-369-493-642	-10-369-493-6	-10-468-091-18	-10-408-	US-10-657-740-9	US-09-990-747-29	-09-935-642-4	-10-408-	6-253-109	-10-100-957A-17	-10-408-765A	US-10-116-275-148	-10-153-668-284	-09-969-034-4	US-10-468-091-20	US-10-226-956-298
Sequence 176081, Sequence 161149,	e 1618	e 692,	መ	e 146696	e 44859,	e 12, Ar	e 2942,	Sequence 3656, Ap	e 2017,	e 6425.	64	7,		64	18	е 23	9	N	4	41	10	e 170,	e 435,	e 14	e 284	equenc	equence 20,	Sequence 298, App

ALIGNMENTS

US-10-657-740-1

Sequence 1, Application US/10657740 Publication No. US20040157289A1 GENERAL INFORMATION:

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APPLICANT: Hanna, Michael
APPLICANT: Hanna, Michael
APPLICANT: Hanna, Michael
APPLICANT: Koretz, Jane F.
APPLICANT: Crone, Donna
APPLICANT: Smith, Susan E.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
FILE REFERENCE: 01794100H406US1
CURRENT APPLICATION NUMBER: US/10/657,740
CURRENT FILING DATE: 2003-09-08
FRIOR APPLICATION NUMBER: US 60/408,680
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P02489
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1)..(173)
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61 ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL
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Pred. No. 1.4e-96;
D; Mismatches 0;
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121

PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS 173

ISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRL 120

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APPLICANT: Salerno, John C.
APPLICANT: Hanna, Michael
APPLICANT: Koretz, Jane F.
APPLICANT: Coretz, Jane F.
APPLICANT: Smith, Susan E.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
FILE REFERENCE: 01794100H406US1
CURRENT APPLICATION NUMBER: US/10/657,740
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: US 60/408,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rattus norvegicus US-10-316-253-113
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                                       ; LENGTH: 173
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-657-740-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/10657740 Publication No. US20040157289A1
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Query Match
                                                                                                                          SOFTWARE: PatentIn version 3.1 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Procter & Gamble Company APPLICANT: Peters, Kevin APPLICANT: Thompson, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 8865M
                                                                                                                                                                   PRIOR FILING DATE: 2002-
NUMBER OF SEQ ID NOS: 18
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TITLE OF INVENTION: Angiogenesis Modulating
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94.8%;
    94.9%;
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Pred. No. 2e-91;
    Score 869;
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      DB 16;
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    Length 173;
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; Sequence 12, Application US/10657740 ; Publication No. US20040157289A1 ; GENERAL INFORMATION:

APPLICANT: Salerno, John C. APPLICANT: Hanna, Michael

APPLICANT:

Koretz, Jane F.

APPLICANT: 'Crone, Donna
APPLICANT: Smith, Susan E.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
FILE REFERENCE: 01794100H406US1

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RESULT 5
US-10-657-740-12
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Anglogenesis Modulating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: The Procter & Gamble Company
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                                                                         181
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                                                                                                                                                121 GKHNERODDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFSGPKVQSGLDAGHSER
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                                                                         AIPVSREEKPSSAPSS 196
                                                                                                AIPVSREEKPTSAPSS 173
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Thompson, Lari
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83.7%;
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Pred. No. 7.1e-89;
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RESULT 7
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US-10-105-427-2
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SEQ ID NO 2
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: Chimeric protein alpha BNAC crystallin with extraordinarily high
TITLE OF INVENTION: chaperone-like activity and a method thereof
FILE REFERENCE: US- 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10105427
Publication No. US20020177192A1
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Best Local Similarity
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CURRENT FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 2
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CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: US 60/408,680
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 196
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Sequence of chimeric
                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                   116
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                                                                                                                                                        56 VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVZIHGKHNERQDDHGYISREFH 115
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                                                                                                                                                                                                                           1 MDVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLFFLSSTISPYYRQ--SLFR--T
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                                                                                       RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS 173
                                                                                                                                    WFDTGLSEMRLEKDRFSVNLDVKHFSPEDLTVKVQDDFVEIHGKHNREQDDHGYISREFH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIPVSREEKPSSAPSS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIPVSREEKPTSAPSS 173
                                                                                                                                                                                                         MDIAIHHPWIRRPFFFFHSPSRLFDQFFGEHLLESDLFP-TSTSLSPFYLRPPSFLRAPS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKHNERODDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFSGPKVQSGLDAGHSER 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKHNERQDDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAER 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISELMTHMWFVMHQPHAGNPKNNPVKVRSDRDKFVIFLDVKHFSPEDLTVKVLEDFVEIH 120
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                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.7%;
83.7%;
                                                                                                                                                                                                                                                                                               75.3%;
                                                                                                                                                                                                                                                                                                                 74.6%;
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                                                                 SADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSABSS 177
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Pred. No. 7.7e-70;
6; Mismatches 22;
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Pred. No. 7.1e-89;
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                                                                                                                                                                                                                                                                                                                                                                    protein alpha
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APPLICANT: Hanna, Michael
APPLICANT: Koretz, Jane F.
APPLICANT: Crone, Donna
APPLICANT: Smith, Susan E.
                                                                                                                                  Matches
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Sig
Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3
LENGTH: 123
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Salerno, John C.
APPLICANT: Hanna, Michael
APPLICANT: Koretz, Jane F.
APPLICANT: Crone, Donna
APPLICANT: Smith, Susan B.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
FILE REFERENCE: 01794100H406US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: US 60/408,680
PRIOR FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/657,740 CURRENT FILING DATE: 2003-09-08
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CURRENT APPLICATION NUMBER: US/10/657,740
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: US 60/408,680
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                            LENGTH: 105
TYPE: PRT
                                                                                                                                                                                                                           ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                   Local
105 DDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTG 149
                                                                                                                              101;
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                                                                                                                                                   Similarity
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                                                       SPYYRQSLFRTVLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQEDFVEIHGKHNERQ 60
                                                                              SPYYRQSLFRTVLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQ 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SREFHRRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSA 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLFRTVLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10657740
No. US20040157289A1
                                                                                                                                Conservative
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                                                                                                                                                   58.0%;
96.2%;
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                                                                                                                              2;
                                                                                                                                              Score 531; DB 10
Pred. No. le-52;
                                                                                                                                Mismatches
                                                                                                                                                                 DB 16;
                                                                                                                              2;
                                                                                                                                                                 Length 105;
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                                                                                                                              0;
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DDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFSGPKIPSG 105

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; LENGTH: 175
; TYPE: PRT
; ORGANISM: Bos t
US-10-657-740-11
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US-10-657-740-11
                                                                          ; TYPE: PRT
; ORGANISM: Homo
US-10-408-765A-405
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APPLICANT: Ghosh, Soumitra
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
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                                                                                                                                     SEQ ID NO 405
LENGTH: 175
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Best Local :
Best Local Similarity Matches 97; Conserv
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                            FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                            APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM FILE REFERENCE: 01794100H406US1
CURRENT APPLICATION NUMBER: US/10/657,740
CURRENT FILING DATE: 2003-09-08
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APPLICANT: Hanna, Michael
APPLICANT: Koretz, Jane F.
APPLICANT: Crone, Donna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP--TSAP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 WIDTGLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99;
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Smith, Susan E.
                                                                                                                                                                                                                                                                                                                                    Gibson, Bradford W.
Taylor, Steven W.
Glenn, Gary M.
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  Conservative
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                54.5%;
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Pred. No. 9.8e-49;
                  Score 489; DB 16;
Pred. No. 1.4e-47;
  Mismatches
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                                       DB 16;
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                                     Length 175;
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  12;
  Gaps
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US-10-226-956-297
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                  Sequence 297, A Publication No.
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
APPLICANT: Joshi, Lokesh
APPLICANT: Seal, Brandon L.
APPLICANT: Seal, Brandon L.
TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
FILE REFERENCE: ASU-1061-US
CURRENT APPLICATION NUMBER: US/10/226,956
CURRENT FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: 60/314,535
PRIOR APPLICATION NUMBER: 60/314,535
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 320
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NUMBER OF SEQ ID NOS: 117
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CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use
FILE REFERENCE: WL-A-018199
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                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                       APPLICANT: Brophy, Colleen APPLICANT: Komalavilas, Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 RRYKLPSNYDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP--TSAP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 WIDTGLSEMRMEKDRESVNIDVKHESPEELKVKVLGDVIEVHGKHEERQDEHGFISREFH 119
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96; Conserv
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                                                                                                                                                                                                 Panitch, Alyssa
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                                                                                                                                                                                                                                                                                      Application US/10226956 o. US20030060399A1
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                                                                                                                                                                                                                            Padmini
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RESULT 14
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US-10-468-091-19
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Sequence 299, Application US/10226956
Publication No. US20030060399A1
GEMERAL INFORMATION:
APPLICANT: Brophy, Colleen
APPLICANT: Komalavilas, Padmini
APPLICANT: Panitch, Alyssa
APPLICANT: Joshi, Lokesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: AU PR3116
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Pa
SEQ ID NO 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Artificial sequence
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RLPPGVDPAAVTSALSPEGVLSI--
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40.1%;
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Pred. No. 1.5e-30;
1; Mismatches 50;
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                                                                                        Matches
                                                                                                        Query Match
Best Local (
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SEQ ID NO 299
LENGTH: 160
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NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K
                                                                                                                                                                                     OTHER INFORMATION: MAP TO CHR21 69.0
OTHER INFORMATION: EXPRESSED IN LIVE, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: SWISSPROT HIT: P02493, EVALUE 2.00e-32
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TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
FILE REFERENCE: ASU-1061-US
CURRENT APPLICATION NUMBER: US/10/226,956
CURRENT FILING DATE: 2002-08-23
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PRIOR APPLICATION NUMBER: 60/314,535
PRIOR FILING DATE: 2001-08-23
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 40.1%;
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                         1 MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
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                                                                                                             Similarity
MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
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RLPPGVDPAAVTSALSPEGVLSI--
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                                                                            36.9%; Dr
100.0%; Pr
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                                                                                 Score 338; DB 14
Pred. No. 7e-31;
0; Mismatches
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Pred. No. 2e-30;
                                                                                                                             DB 14;
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Qy 61 ISE 63
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Db 61 ISE 63

Search completed: September 27, 2004, 13:23:11
Job time : 49 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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916
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2		No.	Result
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791	798	803.5	806.5	816	816.5	829.5	831	839	843	844	844	849.5	850	850	850
86.4	87.1	87.7	88.0	89.1	89.1	90.6	90.7	91.6	92.0	92.1	92.1	92.7	92.8	92.8	92.8
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alpha-crystallin c															

ALIGNMENTS

OÚ.
A, Molecule type: protein A, Residues: 1-152, 'HT', 156-173 <kra> R, Fujii, N.; Satoh, K.; Harada, K.; Ishibashi, Y.</kra>
A; Relevence number: A94388 A; Contents: revisions A; Accession: A94488
submitted to the Atlas, June 1977
A;Residues: 132-135;146-151;158-162;166-173 <dej> A;Residues: the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and monkey sequence of the tryptic peptides were aligned by homology with the bovine and the peptides were aligned by homology with the bovine and the peptides were aligned by homology with the bovine and the peptides were aligned by homology with the bovine and the peptides were aligned by homology with the bovine and the peptides were aligned by homology with the bovine and the peptides were aligned by homology with the bovine and the peptides were aligned by homology with the bovine al</dej>
: A91421
A;TILIE: The amino acid sequence of the A chain of human alpha-crystallin. A;Reference number: A91421; MUID:?6187952; PMID:817940 A;Contents: compositions of tryptic and thermolytic peptides
FEBS Lett. 58, 310-313, 1975
A;Cross-references: GB:S79457; NID:g244474; PIDN:AAB21309.1; PID:g244475
A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Intering Annual Archystathu gene: Conserved features of the 5'-itanking regions in A;Reference number: 156464; MUID:92139443; PMID:1779432 1.Accession
A;Cross-rerences: GB:M35629; NID:g181077; PIDN:AAA52105.1; PID:g181080; GB:M35628; NI R;Jaworski, C.J.; Chepelinsky, A.B.; Piatiqorsky, J.
A; Molecule type; DNA A; Molecule type; DNA
,
A; Title: Isolation and partial characterization of the human alphaA-crystallin gene.
Jaworski, C.J.; Piatigorsky,
A;Cross-references: EWEL:X14789; NID:g28633; PIDN:CAA32891.1; PID:g28634
A; Status: not compared with conceptual translation
A; Title: A pseudo-exon in the functional human alpha-Acrystallin gene.
R;Jaworski, C.J.; Piatigorsky, J. Nature 337, 752-754, 1989
C; Accession: S03344; A45947; I56464; A91421; A94588; JX0351; I39379; JC5690; A02891
C;Species: Homo sapiens (man) C;Date: 27-Nov-1985 #sequence revision 25-Anr-1997 #text change 22-Tin-1999
N;Alternate names: alpha-A-crystallin
RESULT 1

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R;Roquemore, E.P.; Dell, A.; Morris, H.R.; Panico, M.; Reason, A.J.; Savoy, L.A.; W. J. Biol. Chem. 267, 555-563, 1992
A;Title: Vertrbrate lens alpha-crystallins are modified by O-linked N-acetylglucosa A;Reference number: A58.65; MUID:92112709; PMID:1730617
A;Contents: annotation; O-glycosylation
A;Note: O-glycosylation confirmed but not positioned in human protein
A;Rote: Nomose, Y.; Yamasaki, M.; Yamagaki, T.; Nakanishi, H.; Uemura, T.; Tak Biochem. Biophys. Res. Commun. 239, 918-923, 1997
A;Title: The conformation formed by the domain after alanine-155 induces inversion A;Reference number: JC5690; MUID:98042494; PMID:9367870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein A;Residues: 1-173 <FU2> C;Comment: Form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: alpha-crystallin C;Keywords: blocked amino end; eye lens; glycoprotein; phosphoprotein F;1/Modified site: blocked amino end (Met) (probably acetylated) #status | F;12/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) F;162/Binding site: carbohydrate (Ser) (covalent) #status predicted
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A; Title: A partial cDNA sequence corrects the human alpha A-crystallin primary A; Reference number: 139379; MUID:95137069; PMID:7835394
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A;Cross-references: GDB:119074;
A;Map position: 21q22.3-21q22.3
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                                                                                               R;de Jong, W.W.; Nuy-Terwindt, E.C.; Versteeg, M. Biochim. Biophys. Acta 491, 573-580, 1977 A;Tille: Primary structures of alpha-crystallin a chains A;Reference number: A90618; MUID:77158093; PMID:870070
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A;Cross-references: GB:L25781; NID:g531191; PIDN:AAC37570.1; PID:g688439
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                       A; Molecule type: protein
A; Residues: 1-173 < DEJ >
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A;Note:
                                                                            A;Accession: A02901
                                                                                                                                                                                                                                                                                 alpha-crystallin chain
                                                                                                                                                                                                                                                                                                           CYELAA
                                                                                                                                                                                         puna-crystallin chain A - African elephant (tentative sequence);Species: Loxodonta africana (African elephant);Date: 01-Sep-1981 #sequence_revision 27-Nov-1985 #text_change;Accession: A02901
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and sequences
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       89
     alpha-crystallin chain A - C;Species: Macaca mulatta
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: sequence extracted from NCBI A;Note: tentative sequence confirmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: compositions of tryptic peptides and sequences of residues 2-6 and 146-150 R;Parveen, R.; Smith, J.B.; Sun, Y.; Smith, D.L.
J. Protein Chem. 12, 93-101, 1993
A;Title: Primary structure of rabbit lens alpha-crystallins.
A;Reference number: A53871; MUID:93151974; PMID:8427639
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A; Accession: A02896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-crystallin chain A - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 27-Nov-1985 #sequence revision 27-Nov-1985 C;Accession: A02896; B53871
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F;1-168/Product: alpha crystallin chain A, minor form #status experimental
F;12/Modified site: acetylated amino end (Met) #status experimental
F;122/Binding site: phosphate (Ser) (covalent) #status predicted
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Pred. No. 1.4e-77;
5; Mismatches 2
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Pred. No. 1.1e-77;
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Eur. J. Biochem. 53, 237-242, 1975
A;Title: Primary structures of the alpha-crys
A;Reference number: A91230
A;Accession: A02890
A;Molecule type: protein
A;Residues: 1-172 <DEJ>
A;Note: compositions of tryptic peptides and
C;Superfamily: alpha-crystallin
C;Keywords: blocked amino end; eye lens
F;1/Modified site: blocked amino end (Met) (p
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Cavia porcellus (guinea C;Date: 27-Nov-1985 #sequence_revis C;Accession: A02894 R;de Jong, W.W.; Zweers, A.; Goodma in Protides of the Biological Fluid A;Title: Trends in the molecular ev A;Reference number: A94432 A;Accession: A02894 A;Molecule type: protein
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C; Superfamily: alpha
C; Keywords: acetylat
F; 1/Modified site: a
 RESULT 6
CYCPAA
CYCPAA
CYCPAA
alpha-crystallin chain A - springhaas (tentative sequence)
C;Species: Pedetes capensis (springhaas, springhare)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_c
C;Accession: E94432; A02894
C;Accession: E94432; A02894
R;de Jong, W.W.; Zweers, A.; Goodman, M.
In Protides of the Biological Fluids, Proc. 28th Colloq.,
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Keywords: acetylated amino en
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; Date: 27-Nov-1985 #sequence_revision
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J. Biochem. 53, 237-242, 1975
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Pred. No. 2.9e-77;
2; Mismatches 2
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A;Reference number: *I*A;Accession: A02895
A;Molecule type: prot
A;Residues: 1-173 <DE

protein

A; Title: Trends in the molecular

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of,

28th Collog., alpha-crystallin.

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31-Dec-1996

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A;Title: Trends in the molecular evaluation and the molecular evaluations and the molecular evaluation 
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alpha-crystallin chain A - southern American pika C;Species: Ochotona princeps (southern American pik C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 C;Accession: A02895 R;de Jong, W.W.; Zweers, A.; Goodman, M. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides of the Biological Fluids, Proc. 28th C. in Protides 
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A;Accession: A02897
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A; Molecule type: protein A; Residues: 1-173 < DEJ> C; Superfamily: alpha-cryst C; Keywords: acetylated ami F; 1/Modified site: acetyla
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C;Keywords: acetylated amino end; ey
F;1/Modified site: acetylated amino
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A; Residues: 1-173 <DEU>
C; Superfamily: alpha-crystallin
C; Keywords: acetylated amino end; ey
F; 1/Modified site: acetylated amino
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R;de Jong, W.W.; Zweers, A.; Goodman, M.
in Protides of the Biological Fluids, Proc.
A;Title: Trends in the molecular evolution
                                                                                                                                 A;Title: Trends in the molecular evolution of alpha-crystallin. A;Reference number: A94432 A;Accession: F94432
                                                                                                                                                                                      R;de Jong, W.W.; Zweers, A.; Goodman, in Protides of the Biological Fluids,
                                                                                                                                                                                                                             alpha-crystallin chain A - bush baby (tentative sequence)
(;Species: Galago sp. (bush baby)
(;Deceles: JnDec-1991 #sequence_revision 31-Dec-1991 #text_change 31-Dec-1996
C;Accession: F94432; A02898
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C;Species: Perodicticus potto (potto)
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                                     Superfamily: alpha-crystallin; Keywords: acetylated amino end; eye lens; 1/Modified site: acetylated amino end (M
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alpna-crystallin chain A - Cape rock hyrax (tentative sequence)
C;Species: Procavia capensis (Cape rock hyrax)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change
C;Accession: A02902
                                                                                                                                                                                                                                             alpha-crystallin chain A - rat
alpha-crystallin chain A - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Oct-1982 #sequence revision 27-Nov-1985 #text_change 16-Jun-2000
C;Dates: 15-Oct-1982 #sequence revision 27-Nov-1985 #text_change 16-Jun-2000
C;Accession: A02892; A93739; T55370; T70087
C;Accession: A02892; A93739; T55370; T70087
R;de Jong, W.W.; van der Ouderaa, F.J.; Versteeg, M.; Groenewoud, G.; van Ar Eur: J. Biochem. 53, 237-242, 1975
Eur: J. Biochem. 53, 237-242, 1975
A;Title: Primary structures of the alpha-crystallin A chains of seven mamma.
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             A;Note: the compositions of tryptic peptides and sequences of residues 2-6, 13-16, A;Note: the tryptic peptides were positioned by homology with the bovine sequence R;Moormann, R.J.M.; van der Velden, H.M.W.; Dodemont, H.J.; Andreoli, P.M.; Bloemen Nucleic Acids Res. 9, 4813-4822, 1981
A;Title: An unusully long non-coding region in rat lens alpha-crystallin messenger A;Reference number: A93739; MUID:82081811; PMID:6171772
A;Accession: A93739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: alpha-crystallin C;Keywords: blocked amino end; ey F;l/Modified site: blocked amino
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A; Residues: 1-173 < DEU >
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A; Accession: A02892
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A;Title: Trends in the molecular evolution (A;Reference number: A94432
A;Molecular ***
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C;Species: Meriones unguiculatus (Mong
C;Date: 30-Jun-1988 #sequence_revisior
C;Accession: C94432; A02892
R;de Jong, W.W.; Zweers, A.; Goodman,
in Protides of the Biological Fluids;
                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1-173 c/DZ:
C; Superfamily: alpha-crystallin
C; Keywords: alternative splicing
F; 1/Modified site: blocked amino
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A; Cross-references: GB: M96950;
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A;Molecule type: mRNA
A;Residues: 90-172 <RES>
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A;Experimental source: spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lpha-crystallin chain A - Mongolian jird (tentative sequence)
Species: Meriones unguiculatus (Mongolian jird)
Sate: 30-Jun-1988 #sequence_revision 31-Dec-1991 #text_chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: alpha-crystallin; Reywords: alternative splicing;
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PSNVDQSALSCSLSADGMLTFSGPKVQSGLDAGHSERAIPVSREEKPSSAPSS
                                 PSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS 173
                                                                                                                                               MDVTIQHPWFKRALGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSG
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                                                                      ISEVRSDRDKFVIFLDVKHFSPEDLTVKVLEDFVEIHGKHNERQDDHGYISREFHRRYRL
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Pred. No. 2e-76;
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end (Met) (probably acetylated)
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Pred. No. 2e-76;
5; Mismatches
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A;Note: the mouse sequence appears to be identical with the rat se R;King, C.R.; Piatigorsky, J. Cell 32, 707-712, 1983
A;Title: Alternative RNA splicing of the murine alphaA-crystallin A;Reference number: A18860; MUID:83155647; PMID:6187470
                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 11-173 < KI2>
A; Residues: GB:J00376; NID:g192760; PIDN:AAA37471.1; PID:g387134
A; Cross-references: GB:J00376; NID:g192760; DIDN:AAA37471.1; PID:g387134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A02893; A18860
R;King, C.R.; Shinohara, T.; Piatigorsky, J.
Science 215, 985-987, 1982
A;Title: alphaA-crystallin messenger RNA of the mouse lens: more A;Reference number: A02893; MUID:83119896; PMID:7156978
A;Accession: A02893
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A;Residues: 1-173 <DEJ>
C;Superfamily: alpha-crystallin
C;Keywords: alternative splicing;
F;1/Modified site: blocked amino e
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                                                                                                                                                                                                                C;Keywords: acetylated amino (F;1/Modified site: acetylated
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C;Date: 25-Feb-1985 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
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C;Accession: D94432; A02892
R;de Jong, W.W.; Zweers, A.; Goodman, M.
A;Title: Trends in the molecular evolution of alpha-crystallin.
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                                                                                                                                                                                                                                     ;Superfamily: alpha-crystallin;Keywords: acetylated amino end; alternative
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Pred. No. 2e-76;
5; Mismatches
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5; Mismatches
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length:
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1: /cgn2 6/ptodata/2

2: /cgn2 6/ptodata/2

3: /cgn2-6/ptodata/2

4: /cgn2-6/ptodata/2

5: /cgn2-6/ptodata/2

6: /cgn2-6/ptodata/2
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
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           US-09-023-655-1300
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US-09-659-751-69
US-09-690-407-2
US-08-804-198-1
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US-09-891-742-7
US-08-173-508-7
US-08-173-508-7
US-08-173-508-7
US-08-18-6-7
US-08-18-6-7
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US-09-252-991A-11652
US-09-252-991A-11782
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Sequence 1300, Ap
Sequence 1309, Appl
Sequence 3172, Ap
Sequence 5, Appli
Sequence 5, Appli
Sequence 69, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 148, App
Sequence 11652, App
Sequence 11704, Ap
Sequence 11792, Ap
Sequence 11782, Ap
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10.8	10.8	10.8	10.9	10.9	10.9	10.9	11.0	11.0	11.0	11.1	11.1	11.1	11.1	11.1	11.1	11.2	11.2
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Sequence 886, App	Sequence 10170, A	Sequence 9810, Ap	Sequence 15622, A	Sequence 15698, A	Sequence 15729, A	Sequence 15583, A	Sequence 1, Appli	Sequence 2341, Ap	Sequence 2575, Ap	Sequence 11, Appl	Sequence 11, Appl	Sequence 3, Appli	Sequence 11, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 616, App	Sequence 637, App

ALIGNMENTS

RESULT 1 US-09-023-655-1300

Sequence 1300, Applica Patent No. 6607879 GENERAL INFORMATION:

1300, Application US/09023655
o. 6607879

APPLICANT: Cocks, Benjamin G
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilha
TITILE OF INVENTION: COMPOSIT
TITLE OF INVENTION: EXPRESSI

J. Seilhamer COMPOSITION DEXPRESSION

FOR THE DETECTION OF BLOOD CELL

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; CLONE: 932477
US-09-023-655-1300
                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 85-0555
TELEFAX: (650) 85-4166
INFORMATION FOR SEQ ID NO: 1300:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
                                     IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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STATE: CALIFORNIA
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Query Match

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Score 115.6;

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US-09-513-783A-169
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SEQ ID NO 169
LENGTH: 1380
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Giuliano, Kenne
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A Syst
FILE REFERENCE: 97-022-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/513,783A CURRENT FILING DATE: 2000-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (1)..(1380)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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GACCTICTGTGGCCCCAAGATCCAGACTGGCCTGGATGCCACCCA---CGCCGAGCGAGC 323
                                                                                                                                                                                                                                                                   CGGGGTCTCGGAGATCCGGCACACTGCGGACCGCTGGCGCGTGTCCCTGGATGTCAACCA
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                                                        GCTGCCCCCGGTGTGGACCCCACCCAAGTTTCCTCCTCCCTGTCCCCTGAGGGCACACT
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                                                                                                                             GCACGAGGAGCGGCAGGACGAGCATGGCTACATCTCCCGGTGCTTCACGCGGAAATACAC
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Pred. No. 1.2e-20;
0; Mismatches 119
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3172
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NUMBER OF SEQ ID NOS: 10
SEQ ID NO 5
LENGTH: 1379
                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                             Sequence 5, Application US/09553498 Patent No. 6309861
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Best Local
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                                                 APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: Process for the production
FILE REFERENCE: Case 20379
CURRENT APPLICATION NUMBER: US/09/553,498
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: EP99107412.1
PRIOR FILING DATE: 1999-04-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 826
TYPE: DNA
ORGANISM: Homo
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APPLICANT: Giordano,
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                                                                                                                                                                                           APPLICANT: Ambrosius, Doroth APPLICANT: Rudolph, Rainer
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LOCATION: 557..736
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65.0%;
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                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/618,869
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                                                             FEATURE: NAME/KEY: CDS
LOCATION: (392)..(1090)
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FEATURE:
                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                              LENGTH: 1379
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LOCATION: (392)...(1090)
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CCACGGAAAGCACAACGAGCGCCAGGACGACCACGGCTACATTTCCCGTGAGTTCCACCG 197
                                                 TGTGAAGCACTTCTCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTTGTGGAGAGT 137
                                                                                         GCTCAGCAGCGGGGTCTCGGAGATCCGACAGACGGCTGATCGCTGGCGCGTGTCCCTGGA
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                              GCTGGACTCCGGCATCTCTGAGGTTCGATCCGACCGGGACAAGTTCGTCATCTTCCTCGA 77
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Schaeffner, Joerg
Schwarz, Elisabeth
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Pred. No. 2.1e-15;
0; Mismatches 100; Indels
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Pred. No. 2.1e-15;
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RESULT 7
US-08-900-407-2
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; TYPE: DNA
; ORGANISM: Drosophila
US-09-669-751-69
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US-09-669-751-69
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APPLICANT: Hillman, Jenr
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil
APPLICANT: Shab, Purvi
TITLE OF INVENTION: NEW
TITLE OF INVENTION: PRO:
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2,
Patent No. 5
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SEQ ID NO 69
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: P-NI 3864
CURRENT APPLICATION NUMBER: US/09/669,751
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/168,579
PRIOR FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Methods for Identifying Compounds for
TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
TITLE OF INVENTION: Balance and the Perception of Gravity
FILE REFERENCE: P-NI 3864
                                                                               STREET: 3174 Porter Dr
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
 APPLICATION NUMBER:
                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GACGACTTTGTGGAGATCCACGGAAAGCACAACGAGGGCCCAGGACCACGG
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                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08900407
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                                                                                                                                                                                             3174 Porter Dr.
                                                                                                                                                                                                                                                                                                   Corley, Neil C.
Shah, Purvi
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                                                                                                                                                                                                                Incyte Pharmaceuticals,
                                                                                        Diskette
                                                                                                                                                                                                                                                                     PROTEIN
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US/08/900,407
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Pred. No. 5.5e-05;
                                    2.0
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Sequence 7, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Sutton, Kimberly L.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNT
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Best Local Similarity
Matches 115; Conserv
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INFORMATION FOR SEQ ID NO:
           COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,2
FILING DATE: February 21, 1997
CLASSIFICATION: 435
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LIBRARY: ????
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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ADDRESSEE: THOMAS G. PLANT 1501
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                STREET: LILLY CORPORATE CENTER CITY: INDIANAPOLIS
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CLONE: 1362715
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STRANDEDNESS: single
                                                                                                                                                                                                         COUNTRY:
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IBM Compatible
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Pred. No. 0.00011;
0; Mismatches 103; Indels
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sequence 1, Application US/08804198
Patent No. 5945320

GENERAL

INFORMATION:

Burgett, Stanley

APPLICANT:

APPLICANT: APPLICANT: APPLICANT:

CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER

NUMBER OF SEQUENCES:

APPLICANT: ROSTECK, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE

Richardson, Mark A. Rao, Nagaraja R Burgett, Stanley G. Kuhstoss, Stuart A.

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RESULT 9
US-08-804-198-1
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US-08-804-227C-7
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Best Local Similarity
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REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
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NAME/KEY:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                             TGCCGATGGCATGCTGACCTTCTGTGGCCCCAAGATCCAGACTGGCCTGGATGCCACCCA 311
                                                                  CGACGCCCTCGCCGCCC 30394
                                                                                                 CGCCGAGCGAGCCATCC 328
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350..14002
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31329..36071
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20110..31284
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FEATURE:
NAME/KEY:
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NAME/KEY:
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OPERATING SYSTEM: Macintosh 7
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/804,198 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCATION:
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                                                                                                                                                                                                                                                                                                                                              CACCGTGCTGGACTCCGGCATCTCTGAGGTTCGATCCGACCGGGACAAGTTCGTCATCTT
                                                                                       CAGCGCCGGTCTGCTGGGCAGCCCGGCCCAGGGCAACTACGCGGCGGCCAACGCCACCCT 30377
                                                                                                                                                                                                                                                             ACCGGCCGATCACCCGCTGACGGCGTGGTGCACAGCACCGGCGTCCTCGACGACGGCGT 30197
                                                                                                                                                                                                                                                                                          CCTCGATGTGAAGCACTTCTCCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTTGT 131
                                                                                                                                                                                                                                                                                                                        CACCGTGGTCGCCTGCGACGTCTCCGACGCGGACGCCGTCCGCGGACTGCTCGCCGGCAT 30137
                                 CGACGCCCTCGCCGCCC 30394
                                                            CGCCGAGCGAGCCATCC
                                                                                                                  TGCCGATGCCTGACCTTCTGTGGCCCCAAGATCCAGACTGGCCTGGATGCCACCCA 311
                                                                                                                                              CGTCCACCTGGACGAACTCACCCGCGACCTCGACCTGTCGGCGTTCGTCCTCTTCTCCTC 30317
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36155..41830
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                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 2; Length 44377; Pred. No. 0.031;
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RESULT 11
US-09-899-642A-1
; Sequence 1, Application US/09899642A
; Patent No. 6649814
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RESULT 10

GENERAL INFORMATION:

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NAME/KEY: CDS
LOCATION: 81..1673
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-380-420C-1
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,420C
FILING DATE: 12-No. 6300544-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE DOCKET NUMBER: S-21251A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cDNA
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ADDRESSEE: Syngenta Patent Dept.
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
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                                                                              771
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                                                                                                                                                                                                                                      651
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                                     181 TCCCGTGAGTTCCACCGCCGCCTACCGCCTGCCGTCCAACGTGGACC
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GACGACGCCATGGACATGATGGCCAGCTTCTCCGCCGAGGACTTCTTCCCCCAACGCCGCC 830
                                                                                                               GACGACTTTGTGGAGATCCACGGAAAGCACAACGAGCGCCAGGACGACGACGACATT 180
                                                                                                                                                        TTCGGCAACATCTACGCCTCCAAGCAGTTCGCGCACAAGGAGCGCTTCCAGCACGTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: P450ox
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STRANDEDNESS: double
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STATE: NC
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OF INVENTION: Cytochrome P450 Monooxygenases
R OF SEQUENCES: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                     Conservative
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49.6%;
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Pred. No. 0.032;
0; Mismatches 114;
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US-08-173-508-7
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                                Sequence 7, Application US/08173508
Patent No. 5616485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                    GENERAL INFORMATION:
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 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/380,420
FILING DATE: 12-No. 6649814-1999
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-21251A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moller, Birger
TITLE OF INVENTION: Cytochrome P450 Monooxygenases
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA IMMEDIATE SOURCE:
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MEDIUM TYPE: Floppy disk
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                      TCCATCGTCCTCAACGACCACGTCTTCGCCCTCACCGACGGCATCATCGGCACCGTCGCG
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                                                                                                                                                                                                                           GACGACGCCATGGACATGATGGCCAGCTTCTCCGCCGAGGACTTCTTCCCCAACGCCGCC
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ZIP: 27709
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Bartfeld, Daniel
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3054 Cornwallis Road
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0.032;
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US-08-173-508-7
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APPLICATION NUMBER: US/08/173
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1874
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid strandedness: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 11.6%;
Local Similarity 46.0%;
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ATGCCACCCACGCCG 316
                                                              GCGCGGTGCTGGGCGACGAGAAGCTGACCTACGTGGGAGCGTCGTACGGCACCTTCCTGG
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Timothy
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US-08-265-310-7
                                                                                                                        US-08-265-310-7
                                                             Matches 145;
                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 23-DEC-1993 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/265,310
                                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                   FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1821 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: UFILING DATE: 24-JUN-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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STREET: 3000
STREET: 3000
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                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                               LOCATION:
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CCCAGTACGACATGGTGGCGGTCGACCCCCGGGGCGTGGCCCGCAGTGAACCCGTCGAGT 623
                            CCCTCTTCCGCACCGTGCTGGACTCCGGCATCTCTGAGGTTCGATCCGACCGGGACAAGT 61
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                                                             Conservative
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Jenish, David
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                                                                                                                                                                                   sig_peptide
104..244
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                                                                                                                                      mat_peptide
245..1720
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                                                                          11.6%;
46.0%;
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STREPTOMYCES
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                                                                          Score 43; DB 2;
Pred. No. 0.044;
                                                            Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEASES AND IMPROVED STRAINS FOR EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
                                                                                        DB 2;
                                                                                        Length 1821;
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RESULT 14
US-08-951-742-7
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Patent No. 61
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                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 2000/-512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: VSTEM: PC-1222
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/00
FILING DATE: 16-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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APPLICANT:
                                      FEATURE:
                                                     TOPOLOGY: li
                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHOD FOR EXPRESSION OF PROTEINS TITLE OF INVENTION: BACTERIAL HOST CELLS
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   NAME/KEY:
LOCATION:
                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                         ENGTH:
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                                                                                                                         1821 base pairs
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Lawrence T. Malek
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                                                                       linear
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US-07-951-715A-6
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Best Local Similarity 46.0%;
Matches 145; Conservative
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GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                    MEDIUM TYPE: Floppy
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                                                                                                                                               NAME/KEY:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                       ZIP: 10532
                                                                                                         COUNTRY:
                                                                                                                                           CITY: Hawthorne
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                                                                                                           USA
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Evola, Stephen V.
Crossland, Lyle D.
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Dunder, Erik M.
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Launis, Karen L.
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Lewis, Kelly S
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245..1720
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                                                                                                                                                                                  CIBA-GEIGY Corporation
                                                     Floppy disk
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Pred. No. 0.044;
0; Mismatches 170;
   Version #1.30B
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                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (919)541-8615
TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: SDTUILI, W. MUXTAY
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..3621
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3624 base pairs
TYPE: nucleic acid
                                                                                                                                                  1295 CCGAGCGCCCAACTACGAGAGCTACAGCCACCGCCTGAGCCACATCGGCATCATCCTGC
1415 CCATCGGCCCCAA 1427
                                                                                                                                                                                                                            1235 CCTACGAGAGCCCCCGGCCTGCAGCTGAAGGACAGCGAGACCGAGCTGCCCCCCGAGACCA
                                                                                                                                                                                      152 ACGAGCGCCAGGACCACGGCTACATTTCCCGTGAGTTCCACCGCCGCTACCGCCTGC 211
                                                                                                                                                                                                                                                                92 CCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTTGTGGAGATCCACGGAAAGCACA 151
                                                                                                            AGAGCCGCGTGAACGTGCCCGTGTACAGCTGGACCCACCGAGCGCACCGAACCGCACCAACA 1414
                                    TCTGTGGCCCCAA
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optmized cryIB"
/note= "Disclosed in Figure 6."
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Pred. No. 0.067;
O; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                          Length 3624;
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Search completed: September 27, 2004, 13:35:28 Job time : 78 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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372
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                             /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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Cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

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'cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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SUMMARIES
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Result No.	Score 372 315.2	Watch 100.0	* Query Query Match Length DB 100.0 372 17 84.7 531 1	DB 17	ID US-10-657-740-2 US-10-105-427-1
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4	263	70.7		15	US-10-316-253-110
ъ	215.4	57.9		15	US-10-029-386-12881
თ	211	56.7		15	US-10-029-386-26581
7	129.6	34.8		12	US-10-152-319A-1574
8	129.6	34.8		9	US-09-917-800A-1419
9	123.6	33.2			US-09-954-45
10	123.6	33.2		\sim	US-09-960-70
11	123.6	33.2		10	US-09-873-31
12	123.6	33.2		10	US-09-873-36
13	123.6	33.2		13	3 US-10-342-887-686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Publication No. US20040157289A1
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/408,680 PRIOR FILING DATE: 2002-09-06 NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Crone, Donna
APPLICANT: Smith, Susan E.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
FILE REFERENCE: 017941001406US1
CURRENT APPLICATION NUMBER: US/10/657,740
CURRENT FILLING DATE: 2003-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Salerno, John C. APPLICANT: Hanna, Michael APPLICANT: Koretz, Jane F.
                                                                                                                                                                                                                                                                                                                                  LENGTH: 372
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                     y Match 100.0%; Score 372; DB 17; Local Similarity 100.0%; Pred. No. 1.5e-99; nes 372; Conservative 0; Mismatches 0;
121 GACGACTTTGTGGAGATCCACGGAAAGCACAACGAGCCCAGGACGACCACGGCTACATT 180
                                          61 TTCGTCATCTTCCTCGATGTGAAGCACTTCTCCCCCGGAGGACCTCACCGTGAAGGTGCAG
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                                                                                    TTCGTCATCTTCCTCGATGTGAAGCACTTCTCCCCGGAGGACCTCACCGTGAAGGTGCAG 120
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US-10-105-427-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: DNA sequence for chimeric alpha BNAC US-10-105-427-1
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Publication No. US20020177192A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 332; Conserv
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CURRENT APPLICATION NUMBER: US/10/105,427
CURRENT FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 2
SOFTWAKE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Council of Scientific and Industrial Research TITLE OF INVENTION: Chimeric protein alpha BNAC crystallin with extraordinarily high TITLE OF INVENTION: chaperone-like activity and a method thereof FILE REFERENCE: US- 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                         CACGCCGAGCGAGCCATCCCCGTGTCGCGGGAGGAGGAGCCCACCTCGGCTCCCTCGTCC
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92.2%;
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Pred. No. 7.7e-83;
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                                                                     APPLICANT: The Procter & Gamble Company
APPLICANT: Peters, Kevin
APPLICANT: Thompson, Larry
APPLICANT: Wang, Feng
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
     FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(534)
; OTHER INFORMATION:
US-10-316-253-112
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GENERAL INFORMATION:
APPLICANT: The Prooter & Gamble Company
APPLICANT: Peters, Kevin
APPLICANT: Thompson, Larry
APPLICANT: Wang, Feng
APPLICANT: Greis, Kenneth
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Best Local Similarity
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TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
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                                                                                                                     GATGCCACCCACGCGAGCGAGCCATCCCCCGTGTCGCGGGAGAAGCCCCACCTCGGCT
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                        CCCTCGTCCTAA 372
                                                                                   GATGCTGGCCACAGCGAGAGGGCCATTCCCCGTGTCACGGGAGGAGGAGCCCCAGCTCGGCA
                                                                                                                                                                                                                                                                                                     TCCCGTGAGTTCCACCGCCGCCTACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTCT 240
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CCCTCGTCCTGA 534
                                                                                                                                                                    TGCTCCTTGTCTGCGGATGGCATGCTGACCTTCTCTGGCCCCAAGGTCCAGTCTGGCTTG
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87.1%;
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Pred. No. 6.2e-77;
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US-10-029-386-12881
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US-10-029-386-12881
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Best Local S
Matches 290
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 12881
LENGTH: 573
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.:
SEQ ID NO 110
LENGTH: 1271
      Query Match
                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED
TITLE OF INVENTION: EXPRESSION ANALYSIS
FILE REFERENCE: AEOMICA-X-2
                                         FEATURE:

OTHER INFORMATION: MAP TO CHR21.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8

OTHER INFORMATION: WT HIT: AF0268952.1, EVALUE 0.00e+00

OTHER INFORMATION: SWIJSPROT HIT: BF726856.1, EVALUE 0.00e+00

OTHER INFORMATION: SWIJSPROT HIT: P02489, EVALUE 1.00e-32
                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                               TYPE: DNA
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NAME/KEY: CDS
LOCATION: (159)...(749)
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ORGANISM: Rattus
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mes 290; Conserv
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Pred. No. 1.9e-67;
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US-10-029-386-26581
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US-10-029-386-26581
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HUMAN GENOME-DERIVED SINGLE
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
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LENGTH: 211
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CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO CHR21.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8

OTHER INFORMATION: SWISSPROT HIT: P02489, EVALUE 3.00e-36

OTHER INFORMATION: MT HIT: gi14780619, EVALUE 1.00e-113

OTHER INFORMATION: NT HIT: gi14780619, EVALUE 1.00e-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo
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 GAGGAGAAGCCCACCTCGGCTCCCTCGTCCT
                        GAGGAGAAGCCCACCTCGGCTCCCTCGTCCT
                                                                    GIGGACCAGICGCCCTCTCTCCCCCCTGTCTGCCGATGGCATGCTGACCTTCTGTGGC
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                                                                                                                                                                                                                                                                                                   Score 211;
Pred. No.
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3e-52;
211
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GENERAL INFORMATION:

Sequence 1574, Application US/10152319A Publication No. US20040072160A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1574
LENGTH: 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
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PRIOR
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APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/330,867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-07-10
APPLICATION NUMBER: US 60/303,807
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                                       GCCGAGCGAGCCATCCCCGTGTCGCGGGAGGAGGAAGCC
CCTGAGCGCACCATTCCCATCACCCGTGAAGAGAAGCC 500
                                                                                TCGGATGGAGTCCTCACTGTGAATGGACCAAGGAAACAG
                                                                                                                                                                  CACAGGAAGTACCGGATCCCAGCCGACGTGGATCCTCTCACCATTACTTCTTCCCTGTCA 414
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64.2%;
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Pred. No. 2.8e-28;
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; OTHER INFORMATION: Genbank Accession No. US20020119462A1 M55534 US-09-917-800A-1419
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PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 20001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR PILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR PILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/298,884
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PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1419
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Best Local Similarity 64.2%;
Matches 217; Conservative
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CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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TITLE OF INVENTION: Molecular Toxicology Modeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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ORGANISM: Rattus norvegicus
FEATURE:
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1045
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CCTGAGCGCACCATTCCCATCACCCGTGAAGAGAAGCC 1082
                                           GCCGAGCGAGCCATCCCCGTGTCGCGGGAGGAGAAGCC
                                                                                             TCGGATGGAGTCCTCACTGTGAATGGACCAAGGAAACAG
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Castle, Arthur
Elashoff, Michael
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Pred. No. 3.1e-28;
0; Mismatches 109;
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RESULT 10
US-09-960-706-869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/60/234,952
PRIOR FILING DATE: 2000-09-20
PRIOR PPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR PLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR PPLICATION NUMBER: US/60/235,637
PRIOR PPLICATION NUMBER: US/60/235,637
PRIOR PPLICATION NUMBER: US/60/235,638
PRIOR PPLICATION NUMBER: US/60/235,638
PRIOR PPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,711
                 GENERAL INFORMATION:
APPLICANT: Munger, william E.
APPLICANT: Munger, william E.
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-01US
                                                                                                                         Sequence 869, Application US/09960706 Publication No. US20030134280A1
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Best Local Similarity
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TITLE OF INVENTION: Process
TITLE OF INVENTION: Sets
    CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 2276
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PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
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CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
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LENGTH: 691
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FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                             TTCCACCGCCGCTACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTCTTGCTCCCTG
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  NUMBER:
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US/09/960,706
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Pred. No. 1.7e-26;
0; Mismatches 99;
                                                         Diagnosis of Benign Prostatic Hyperpla
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10 CGCACCGTGCTGGACTCCGGCATCTCTGAGGTTCGATCCGACCGGGACAAGTTCGTCATC

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APPLICANT: Munger, William E.
APPLICANT: Kulkarni, Prakash
APPLICANT: Kulkarni, Prakash
APPLICANT: Getzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Waga, Iwao
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Hyperplasia Using Gene Ex
FILE REFERENCE: 44921-5029-US
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT APPLICATION NUMBER: US/09/873,319A
CARLIER APPLICATION WUMBER: US/09/873,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
COUNTMENT: Drafts VOC.
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US-09-873-319-566
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                                                                       ; OTHER INFORMATION: Genbank Accession No. US20030134324A1 S45630 US-09-873-319-566
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                                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 566
 Matches
                  Query Match
Best Local S
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Best Local :
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PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 09/873,319
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                         LENGTH: 691
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                             FEATURE:
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tch 33.2%; al Similarity 64.9%; 183; Conservative
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o. US20030134324A1
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Score 123.6;
Pred. No. 1.7e
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Pred. No. 1.7e-26;
0; Mismatches 99;
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Gene Expression Profiles
 1.7e-26;
nes 99;
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RESULT 12
US-09-873-367C-764
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APPLICANT: Soppet, Dani
APPLICANT: Endress, Gra
APPLICANT: Augustus, M
APPLICANT: Ebner, Reinl
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Best Local Similarity
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT ELING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR FILING DATE: 2000-11-01
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ORGANISM: Homo sapiens
-09-873-367C-764
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Ebner, Reinhard
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Endress, Gregory
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TITLE OF INVENTION: Diagnosis and Prognosis of FILE REFERENCE: 9301-188-999
CURRENT APPLICATION UNMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION UNMBER: 60/298,918
PRIOR PILING DATE: 2001-66-18
PRIOR APPLICATION UNMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 686
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US-10-342-887-686
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                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                            APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
                                                                                                                                                                                                                                                         Sequence 686, Application US/10172118 Publication No. US20030224374A1
                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT:
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis
FILE REFERENCE: 9301-175-999
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256

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Sequence 61, Application US/10133937
Publication No. US20030207278A1
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
TITLE OF INVENTION: OTHER BIOLOGICAL STATES
FILE REFERENCE: 11613.56US01
CURRENT APPLICATION NUMBER: US/10/133,937
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61
LENGTH: 691
TTPE: DNA
ORGANISM: Homo sapiens
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US-10-133-937-61
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Best Local Similarity
Matches 183; Conserv
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CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 686
LENGTH: 691
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Best Local Similarity
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
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                                TTCCTCGATGTGAAGCACTTCTCCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTT 129
                                                                      CCCAGCTGGTTTGACACTGGACTCTCAGAGATGCGCCTGGAGAAGGACAGGTTCTCTGTC
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Pred. No. 1.7e-26;
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Pred. No. 1.7e-26;
0; Mismatches 99
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                                TCTGCCGATGGCATGCTGACCTTCTGTGGCCCCAAGATCCAG
                                                                 TTCCACAGGAAATACCGGATCCCAGCTGATGTAGACCCTCTCACCATTACTTCATCCCTG
TCATCTGATGGGGTCCTCACTGTGAATGGACCAAGGAAACAG
                                                                                                TTCCACCGCCGTACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTCTTGCTCCCTG 249
478
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Search completed: September 27, 2004, 14:39:44
Job time : 3846 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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372
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Length DB ID 531 7 ABX 531 7 ABX 538 9 ADB 528 9 ADB 528 9 ADB 528 9 ADB 527 9 ADE 691 6 ABK 691 6 ABK 691 6 ABT 691 6 ABT 691 6 ABT 691 6 ABT 691 3 AAC 691 3 AAC 911 3 AAC 913 3 AAC 914 3 AAC 917 ABX 575 6 ABO
ABX ABIT ABBY ADB ABT ADB ABT ADB
ID ABX12062 AD852521 AB741872 AD852642 AD852642 AD8526374 AD8575374 AD8575375 AD8575376 ABX10966 ABL62427 ABB10966 ABL62427 ABB10966 ABK6671 AAC10867 ABC10863 AAC10863 AAC10863 AAC10863 AAC10863 AAC10862 AAC10861 AAC3893 AAC10862 AAC10861 AAC38974 ABZ35338 ABS38978 ABX38978

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96.4	96.4	98.6	100.4	101.2	102.6	102.8	103.4	104.6	106.8	106.8	110	114.4	115	115.6	115.6	115.6	115.6	115.6	115.6	115.6	O T T G
		26.5	27.0				27.8	28.1	28.7	28.7	29.6	30.8	30.9	31.1	31.1	31.1	31.1		31.1	31.1	5 I
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ABL63995	ABL63575	AAL19387	ACH16863	ABL99507	ABX47457	ACH17737	ABK87386	ABL07843	AAS56378	ABT41710	ACH34922	AAZ42230	AAC03894	ABS71560	AAA93441	ADD70998	ABN97370	ABQ60780	AAQ48718	ABV94670	AAC/6681
Ab163995	Ab163575	Aal19387	Ach16863	Ab199507	Abx47457	Ach17737	Abk87386	Ab107843	Aas56378	Abt41710	Ach34922	Aaz42230	Aac03894	Abs71560	Aaa93441	Add70998	Abn97370	Abq60780	Aaq48718	Abv94670	Aac76681
Breast ca	Breast ca	Human bre	Human adu	Target ca	Bovine ES	Human adu				Toxicity	Human end		Human sec	DNA encod	GFP-HSP27	Human hea	Gene #386	Human HSB	Encod	Human pan	. Human ORF

ALIGNMENTS

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RESULT 1
ABX12062
ID ABX1
XX ABX1
AC ABX1
AC ABX1
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Incr
XW I
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                                                                                                                                                                         26-MAR-2002; 2002US-00105427
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Synthetic.
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(KUMA/) KUMAR L V S. (RAOC/) RAO C M.
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/note= "Derived from DNA sequence encoding N-terminal
sequence of alpha B crystallin"
248. .531
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/note= "Derived from DNA sequence encoding N-terminal
sequence of alpha A crystallin"
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1. .247
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RESULT 2
ADB252521
ID ADB8
XX
AC ADB8
XX
XX
DT 04-1
XX
DE Prin
XX
KW tox
KW tox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 531 BP; 90 A; 198 C; 130 G; 113 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                   toxic effect; gene expression profile; hepatotoxicity; diagnostic marker; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                                                                                        04-DEC-2003
                                                                                                              Primary rat hepatocyte toxicity modelling related gene SEQ ID
                                                                                                                                                                                                                                 ADB52521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 9; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGAGATCCACGGAAAGCACAACGAGCGCCAGGACGACCACGGCTACATTTCCCGTGAG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCAGCTGGTTTGACACTGGACTCTCAGAGATGCGCCTGGAGAAGGACAGGTTCTCTGTC
                                                                                                                                                                                                                                 standard; DNA; 1056 BP
                                                                                                                                                                                                                                                                                                                            CACGCCGAGCGAGCCATCCCCGTGTCGCGGGAGGAGAAGCCCACCTCGGCTCCCTCGTCC
                                                                                                                                                                                                                                                                                                                                                  CACGCCGAGCGAGCCATCCCCGTGTCGCGGGAGGAGAAGCCCACCTCGGCTCCCTCGTCC 369
                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGCCGATGGCATGCTGACCTTCTGTGGCCCCAAGATCCAGACTGGCCTGGATGCCACC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCCACCGCCACCGCTACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTCTTGCTCCCTG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGAGATCCACGGAAAGCACGACGACGACGACCACGGCTACATTTCCCGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                        TCTGCCGATGCCATGCTGACCTTCTGTGGCCCCAAGATCCAGACTGGCCTGGATGCCACC
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Pred. No. 2.2e-62;
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Best Local 9
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22-APR-2002;
08-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-APR-2002;
11-APR-2002;
19-APR-2002;
                                                                                                                                                                                                                                                                                                          The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present semiger to recent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2002;
13-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAY-2002;
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10-APR-2002;
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Elashoff M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-2002;
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                                                                                                                                                                                                                                                     Sequence 1056 BP; 199 A; 333 C; 269 G; 255 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                   drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 44; SEQ ID NO 3063; 874pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mean values.
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NY-2002; 2002US-0378370P-
NY-2002; 2002US-0378652P-
NY-2002; 2002US-0378653P-
NY-2002; 2002US-0378665P-
H-2002; 2002US-0394253P-
H-2002; 2002US-0394253P-
NP-2002; 2002US-0407688P-
NP-2003; 2002US-0442900P-
                             121
                                                                                                                            163
                                                                                                                                                                                         324;
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                                                                                                                                                                                                          Similarity
                                                                                                                          TCTCTCTTCCGCACAGTGTTGGACTCCGGCATCTCTGAGGTCCGATCTGACCGGGACAAG
                             GACGACTTTGTGGAGATCCACGGAAAGCACGACGACGACGACGACCACGGCTACATT
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GAAGATTTCGTGGAGATCCATGGCAAACACAACGAGAGGCAGGATGACCATGGCTACATT
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2002US-0371135P.
2002US-0371150P.
2002US-0371413P.
2002US-0373601P.
                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-0363534P
                                                                                                                                                                                                          79.4%;
87.1%;
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                                                                                                                                                                                           0
                                                                                                                                                                                                          Score 295.2; DB 9
Pred. No. 8.4e-58;
                                                                                                                                                                                           Mismatches
                                                                  ACTTOTOTOTGAGGACOTCACCGTGAAGGTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Higgs B,
                                                                                                                                                                                                                            DB 9;
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10-JUL-2001;

28-AUG-2001;

27-SEP-2001;

27-SEP-2001;

21-NOV-2001;

10-DEC-2001;

19-DEC-2001;

19-DEC-2001;

21-FEB-2002;

21-FEB-2002;

21-FEB-2002;
                                                                                                  Predicting
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                                                           dicting at least of the seling, comprises plants of the selection of the s
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2001US-0324928P.
2001US-0330462P.
2001US-0330867P.
2001US-0336149.
2001US-0340873P.
2002US-0357842P.
2002US-0357843P.
2002US-0357843P.
2002US-0357843P.
2002US-0364134P.
2002US-0364134P.
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2002US-0370247P.
2002US-0372794P.
2002US-0371679P.
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2001US-0303807P.
2001US-0303808P.
2001US-0303810P.
                                         database.
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2001US-0297523P.
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                                                                                                                                                                                                                                  INC.
                                                         one toxic effect preparing a gene to the compound,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression profile; renal toxicity; toxicity marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related
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                                                                                                                                                                                        Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxicity assay; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rat gene SEQ ID No 1574.
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                                                                                                                                                                                    Higgs
                                                    of a compound, useful for toxicity expression profile of a tissue or and comparing the gene expression
                                                                                                                                                                               В,
                                                                                                                                                                                        Castle
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Example

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Page;

446pp;

English

04-FEB-2002; 2002US-0353171P 13-MAR-2002; 2002US-0363534P 04-FEB-2003; 2003WO-US003482

14-AUG-2003

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RESULT 4
ADB52642
ID ADB5
XX ADB5
XX ADB5
XX Prim
XX Prim
XX COX1
KW COX1
KW Prim
XX Prim
XX Ratt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The invention relates to a novel method of predicting at least one toxic CC effect of a compound. The method comprises a gene expression profile of a CC tissue or cell sample exposed to the compound, and comparing the gene CC expression profile to a database comprising at least part of the data or CI information given in the specification. The methods are useful for CC predicting at least one toxic effect of a compound, predicting the renal CC confectly of a compound, or identifying toxicity markers in tissues or CC cells exposed to known renal toxin. The genes are useful as toxicity CC markers in drug screening and toxicity assays, in monitoring disease or CC physiological states, or disease progression. This polynucleotide CC represents a rat DNA sequence relating to the toxic database CC described in the specification. NOTE: The sequence data for this patent CC cells exposed to form part of the printed specification, but was obtained in CC electronic format directly from the World Intellectual Property
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Best Local (
                                                                                                                                                                                                                                                                                                                                                  ADB52642 standard;
                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                  primary
                                                                                                                                                                                                                   toxic effect;
                                                                                                                                                                                                                                               Primary rat hepatocyte toxicity modelling
                                                                                                                                                                                                                                                                                    04-DEC-2003
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                                                                                                                                                                                                toxicity marker; toxicity progression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                 rat hepatocyte toxicity modelling; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGAGCGCACCATTCCCATCACCCGTGAAGAGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGAGCGAGCCATCCCCGTGTCGCGGGAGGAGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCGCCGCTACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTCTTGCTCCCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGATCCACGGAAAGCACAACGAGCGCCAGGACGACGACGGCTACATTTCCCGTGAGTTC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCGATGTGAAGCACTTCTCCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACGACTTTGTG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCGTGCTGGACTCCGGCATCTCTGAGGTTCGATCCGACCGGGACAAGTTCGTCATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGGATGGAGTCCTCACTGTGAATGGACCAAGGAAACAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACAGGAAGTACCGGATCCCAGCCGACGTGGATCCTCTCACCATTACTTCTTCCCTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGTGCACGCCAAGCACGAAGAGCGCCCAGGACCAACATGGCTTCATCTCCAGGGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGACGTGAAGCACTTCTCTCCAGAGGAACTCAAAGTCAAGGTTCTGGGAGACGTGATT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTGGATTGACACTGGGCTCTCAGAGATGCGTATGGAGAAGGACAGGTTCTCTGTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                 gene expression profile;
                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.8%;
64.2%;
                                                                                                                                                                                                                                                                                                                                                    ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 129.6; DB 7;
Pred. No. 3.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                              hepatotoxicity;
                                                                                                                                                                                                drug screening;
                                                                                                                                                                                                                                               related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109;
                                                                                                                                                                                                                                                                                                                                                                                                                                   500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350
                                                                                                                                                                                  ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                SEQ ID NO:3184.
                                                                                                                                                                                                              diagnostic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Best Local :
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11-APR-2002;
19-APR-2002;
19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-2002;
10-APR-2002;
10-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 44; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-731472/69
                                                                                                                                                                                                                                                                                                                                                                                                                    toxicity modelling related gene sequence from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE
                                                                                                                                                                                                                                                                                                                                         local Similarity
                                                                                            193
                               253
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                                                                                                                                                            GAGATCCACGGAAAGCACAACGAGCGCCAGGACGACCACGGCTACATTTCCCGTGAGTTC 192
                                                                                                                                                                                                                           CTCGATGTGAAGCACTTCTCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTTGTG 132
                                                                                                                                                                                                                                                                                      ACCGTGCTGGACTCCGGCATCTCTGAGGTTCGATCCGACCGGGACCAAGTTCGTCATCTTC
                                                                                                                                                                                                                                                                                                                                                                                        528
                              CTGGACGTGAAGCACTTCTCCCAGAGGAACTCAAAGTCAAGGTTCTGGGAGACGTGATT
 TCGGATGGAGTCCTCACTGTGAATGGACCAAGGAAACAG-
                                                                                              CACCGCCGCTACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTCTTGCTCCCTGTCT
                                                                                                                             GAGGTGCACGGCAAGCACGAAGAGCGCCAGGACGAACATGGCTTCATCTCCAGGGAGTTC
                                                                                                                                                                                                                                                          AGCTGGATTGACACTGGGCTCTCAGAGATGCGTATGGAGAAGGACAGGTTCTCTGTGAAC 234
                                                               CACAGGAAGTACCGGATCCCAGCCGACGTGGATCCTCTCACCATTACTTCTTCCCTGTCA
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2002US-0378652P.
2002US-0378655P.
2002US-0378665P.
2002US-0394253P.
2002US-0394254
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2002US-0371134P.
2002US-0371135P.
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                      B₽;
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2002US-0374139P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO 3184; 874pp; English
                                                                                                                                                                                                                                                                                                                                                                                      114 A; 170 C; 128 G; 116 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC.
                                                                                                                                                                                                                                                                                                                                         34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johnson
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                         Score 129.6; DB 9 Pred. No. 3.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ζ,
                                                                                                                                                                                                                                                                                                                           Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Castle A,
                                                                                                                                                                                                                                                                                                                          Indels 12;
                                                                                                                                                                                                                                                                                                                                                      Length 528;
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463
CCTGAGCGCACCATTCCCATCACCCGTGAAGAGAAGCC
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31-JUL-2000;
02-NOV-2000;
11-MAY-2001;
15-MAY-2001;
22-MAY-2001;
06-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening; differential expression; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                             07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                      09-JUL-2001;
                                                                                                                                                                                                                                           13-JUN-2001;
19-JUN-2001;
                                                                                                                                                                                                                                                                                                30-JUL-2001; 2001WO-US023872
                                                                                                                                                                                                                                                                                                                         WO200210453-A2
                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                          ABK63512;
                                                                                                                                                                                                                                                                                                                                                                                                      ABK63512
                                                                                                                                                                                                                           (GENE-) GENE
                                                                                                                                                                                                                                                                                                                                                                                                      standard; cDNA;
                                                                                                                                                                                                                                     2000US-0222040P.

2000US-0244880P.

2001US-0290029P.

2001US-0290645P.

2001US-0292336P.

2001US-029735P8P.

2001US-029745P9.

2001US-029745P9.

2001US-0303459P.
                                                                                                                                                                                                                           LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                  differentially expressed
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      1247
                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                   in
                                                                                                                                                                                                                                                                                                                                                                   response to a hepatotoxin #1419
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for

Mendrick 'n Porter MW, Johnson KR, Castle AL, Elashoff MR;

WPI; 2002-241625/29

Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed

Claim 1; SEQ ID NO 1419; 239pp; English

Gaps

294

cc cells. Also included are methods of predicting at least one toxic effect
CC cells. Also included are methods of predicting at least one toxic effect
CC of a compound or progression of a toxic effect, preferably the
CC hepatotoxicity of a compound, comprising detecting the level of
CC expression in a tissue or cell sample exposed to the compound of two or
CC more genes listed in the specification, where differential expression of
CC the genes is indicative of at least one toxic effect or progression. The
CC method can also be used to identify an agent which modulates the toxic
CC response and predict cellular pathways that a compound modulates in a
CC cell. The methods utilise a set of at least two probes (on a solld
CC support in kit form), where each of the probes comprises a sequence that
CC specifically hybridises to a gene listed in the specification, a computer
CC system comprising a database containing information identifying the
CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
CC set of genes comprising at least two genes listed in the specification,
CC and a user interface to view the information used to present information
CC identifying the expression level in a tissue or cell of at least one gene
CC sisted in the specification. The method is used to present information global
CC hence in means a provided to the method is useful for elucidating global The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and expression information may be used as diagnostic markers the

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313

GCCGAGCGAGCCATCCCCGTGTCGCGGGAGGAGGAAGCC 350

GCCTCTGGC

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ADE75374
ID ADE75
XX ADE7
XX ADE7
XX ADE7
XX Humm
XX Hybi
KW Hybi
KW SHSi
KW Proi
KW Proi
KW Proi
KW Proi
KW Hom
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Best Local
                           23-APR-2003; 2003WO-GB001721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybrid protein chaperone; protein stabilisation; heat shock protein; sHSP family; protein aggregation inhibition; cell death inhibition; genome stability pathway inhibition; protein denaturation identification;
                                                                                                                                                                                                                                                                mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human mutant alphaB-crystallin fragment-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prediction or identification of the physiological state of tissue or sample that has been exposed to a compound or agent. Hepatotoxicity: characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gewhich is differentially expressed in response to a hepatotoxic agent
                                                                                                                                 WO2003091266-A2
                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein conformation related disease; cardiomyopathy; cataract; neurodegenerative disease; cardiant; ophthalmological; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE75374 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGACGTGÄÄĞCÄCTTCTCTCCAGAGGÄACTCAAAGTCAAGGTTCTGGGAGÄCGTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACAGGAAGTACCGGATCCCAGCCGACGTGGATCCTCTCACCATTACTTCTTCCCTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCGCCGACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTCTTTGCTCCCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGATGTGAAGCACTTCTCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTTGTG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCGTGCTGGACTCCGGCATCTCTGAGGTTCGATCCGACCGGGACAAGTTCGTCATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTGGATTGACACTGGGCTCTCAGAGATGCGTATGGAGAAGGACAGGTTCTCTGTGAAC 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alphaB-crystallin; wild-type; human; cassette mutagenesis;
                                                                                                                                                                                                                                                           /note= "Unique
replace(497,T)
                                                                                                                                                                                                            /*tag=
/note=
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
493. .498
                                                                                                                                                                                   mique
                                                                                                                                                                                                                                                                                                                  *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.8%;
                                                                                                                                                                                   "Mutagenesis to G
AvaI site between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВÞ
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Pred. No. 3.
                                                                                                                                                                                                                                                                                         AvaI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 109;
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                                                                                                                                                                                bases
                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                         from T
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                                                                                                                                                                                                                                                                                       casette
                                                                                                                                                                                T at this site generates 493-498"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 936
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correplacement of one or more regions of an sHSP with the corresponding of region from a second sHSP can improve the activity compared to native SHSPs. In a particual rembodiment of the invention, the hybrid chaperone of sHSPs. In a particual rembodiment of the invention, the hybrid chaperone of sHSPs. In a particual rembodiment of the invention, the hybrid chaperone of shaperone of the invention can comprise of family. The invention also encompasses methods for stabilising proteins of such as enzymes, therapuetic proteins, diagnostic proteins, reporter of proteins or antibodies, their fragments or conjugates in an aqueous solution using hybrid protein associated with the above hybrid protein comprising at least one protein associated with the above hybrid protein chaperone; nucleic acids and vectors encoding a hybrid protein chaperone; cand the coexpression of a recombinant protein of interest and a hybrid protein chaperone; cand the coexpression of a recombinant protein of interest and a hybrid protein chaperone; cand the coexpression of a recombinant protein state and a hybrid protein chaperone; cand the coexpression of a recombinant protein state and a hybrid protein chaperone; or identification of proteins that are in the correct protein conformations (e.g., cardiomyopathies, cataracts or the treatment of such diseases), or for the manufacture of a medicament for the treatment of such diseases), or for the manufacture of a medicament for the treatment of such diseases). The present sequence represents a mutant can the form of fee ADE75375) to generate a unique Aval restriction site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins and/or protein activities. Protein chaperones (also known as heat shock proteins) are divided into 4 families on the basis of their primary sequence and chaperone properties: HSP90, HSP70, HSP60 and sHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hybrid protein chaperone (e.g. heat shock protein) useful for stabilizing proteins and/or protein activities, or as an agent to prevent protein aggregation, or for treating diseases involving altered protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (small heat shock protein). The invention is based upon the finding that among the sHSP family, which have a general structure of a cenral domain (called the alpha-crystallin domain) flanked by N and C-terminal regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a hybrid protein chaperone for stabilising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 12; 45pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002; 2002GB-00009334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VINU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and sHSP
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Sequence 537 BP; 118 A; 171 C; 125 G; 123 Η, 0 ٦, 0 Other;

DΒ

9;

Length 537;

ed from T (see ADE75375) to generate a unique Aval restriction 31e was used for subsequent cassette mutagenests (along with a vector-SacI site) to introduce heterologous C-terminal sequences onto

alphaB-crystallin.

멍 Ś 멂 Ś 밁 Ś 밁 Ş Best Loc Matches Local 360 250 TCTGCCGATGCCATGCTGACCTTCTGTGGCCCCAAGATCCAGACTGGCCTGGATGCCACC 240 AACCTGGATGTGAAGCACTTCTCCCCAGAGGAACTCAAAGTTAAGGTGTTGGGAGATGTG 180 215; 70 10 Similarity TTCCACAGGAAATACCGGATCCCAGCTGATGTAGACCCTCTCACCATTACTTCATCCCTG TTCCACCGCTACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTCTTGCTCCCTG ATTGAGGTGCATGGAAAACATGAAGAGCGCCAGGATGAACATGGTTTCATCTCCAGGGAG TTCCTCGATGTGAAGCACTTCTCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTT CCCAGCTGGTTTGACACTGGACTCTCAGAGATGCGCCTGGAGAAGGACAGGTTCTCTGTC Conservative 33.5%; 63.0%; 0 Score 124.6; Pred. No. 4.0 Mismatches 4.6e-19; 114; Indels 12; Gaps 309 299 129 69 249 359 189 239

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TCATCTGATGGGGTCCTCACTGTGAATGGACCAAGGAAACAG--

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            CC proteins and/or protein activities. Protein chaperones (also known as comparing the shock proteins) are divided into 4 families on the basis of their CC primary sequence and chaperone properties: HSP90, HSP70, HSP60 and sHSP CC (small heat shock protein). The invention is based upon the finding that CC (among the sHSP family, which have a general structure of a central domain CC (called the alpha-crystallin domain) flanked by N and C-terminal regions, CC replacement of one or more regions of an sHSP with the corresponding CC region from a second sHSP can improve the activity compared to native CC sHSPs. In a particualr embodiment of the invention, the hybrid chaperone CC is a hybrid sHSP designated alphab-HSP27 comprising the N-terminus and CC central portion of alphab-crystallin and the C-terminal tail of HSP27. CC regions from HSP90, HSP70 and HSP60 families as well as from the sHSP C family. The invention also encompasses methods for stabilising proteins CC such as enzymes, therapuetic proteins, diagnostic proteins, reporter CC proteins or antibodies, their fragments or conjugates in an aqueous consultion using hybrid protein chaperones; stabilised protein formulation CC comprise consultion using hybrid protein chaperones; stabilised protein formulation consultions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybrid protein chaperone; protein stabilisation; heat shock protein; sHSP family; protein aggregation inhibition; cell death inhibition; genome stability pathway inhibition; protein denaturation identification; protein conformation related disease; cardiomyopathy; cataract; neurodegenerative disease; cardiant; ophthalmological; neuroprotective; gene therapy; alphaB-crystallin; wild-type; human; cassette mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hybrid protein chaperone (e.g. heat shock protein) useful for stabilizing proteins and/or protein activities, or as an agent to protein aggregation, or for treating diseases involving altered p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2002; 2002GB-00009334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-2003; 2003WO-GB001721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003091266-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human wild-type alphaB-crystallin fragment-encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE75375 standard; DNA; 537 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a hybrid protein chaperone for stabilising
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 12; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-865571/80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYDU-)
comprising at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
  least one protein associated with the above hybrid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Mutagenesis of T to G at this site generates unique AvaI site between bases 493-498"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replace(497,G)
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chaperone; nucleic acids and vectors encoding a hybrid protein chaperone; and the coexpression of a recombinant protein of interest and a hybrid protein chaperone. The hybrid protein finiterest and a hybrid protein chaperones are useful as agents to prevent protein aggregation, as inhibitors of cell death and genome stability pathways, for identification of proteins that are in the process of unfolding, for the treatment of diseases involving altered protein conformations (e.g., cardiomyopathies, cataracts or neurodegenerative diseases, or for the manufacture of a medicament for the treatment of such diseases. The present sequence represents a wild-type human alphabacrystallin DNA sequence. The T at position 497 was mutated to G (see ADE75374) to generate a unique Aval restriction site
                                           10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 537 BP; 118 A; 171 C; 124 G; 124 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alphaB-crystallin.
                                                                                                                                                                                                                                                                              prostate cancer;
                                                                                                                                                                                                                                                                                           breast cancer; colon cancer; gastric
                                                                                                                                                                                                                                                                                                  Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer;
                                                                                                                                                                                                                                                                                                                                          Renal cancer associated gene
                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX39668
                                                                                                                                                        15-JUL-1998;
                                                                                                                                                                                     28-JAN-1999
                                                                                                                                                                                                                    WO9904265-A2
                                                                                                                                                                                                                                                 Homo sapiens
              (LUDW-) LUDWIG
                                                                                                       10-OCT-1997
                                                                                                                         17-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was used for subsequent cassette mutagenesis (along with a vector-
SacI site) to introduce heterologous C-terminal sequences onto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
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                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCCACAGGAAATACCGGATCCCAGCTGATGTAGACCCTCTCACCATTACTTCATCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGAGATCCACGGAAAGCACAACGAGCGCCAGGACGACGACGGCTACATTTCCCGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCTGGATGTGAAGCACTTCTCCCCAGAGGAACTCAAAGTTAAGGTGTTGGGAGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCAGCTGGTTTGACACTGGACTCTCAGAGATGCGCCTGGAGAAGGACAGGTTCTCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCACCGTGCTGGACTCCCGGCATCTCTGAGGTTCGATCCGACCGGGGACAAGTTCGTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGCCGATGGCATGCTGACCTTCTGTGGCCCCAAGATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTGAGGTGCATGGAAAACATGAAGAGCGCCAGGATGAACATGGTTTCATCTCCAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCCTCGATGTGAAGCACTTCTCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATCTGATGGGGTCCTCACTGTGAATGGACCAAGGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCACCGCCTACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTCTTGCTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                TSNI
                                                           97US-00948705
97GB-00021697
                                                                                            97US-0061599P.
97US-0061765P.
                                                                                                                         97US-00896164
                                                                                                                                                          98WO-US014679
                                               98US-00102322.
                CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 123.6;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                cancer; renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 Other;
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                                                                                                                                                                                                                                                                                              human;
lung c
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Best Local S
Matches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product complexed with an HLA molecule; and the expression product as a interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule, and (b) determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Old LJ,
O'hare
                                                                                     cytostatic;
                                                                                                  stomach;
                                                                                                                                                                                                                    ABL65204 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                  15-MAY-2002
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                                                                                                                                        cancer
                                               sapiens.
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                                                                                                             cancer;
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                                                                                               lung;
                                                                                                                                                                                                                                                                                                                                                                                                           GTGGAGATCCACGGAAAAGCACGACGACGACGACGACGACGACGATTTCCCGTGAG
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                                                                                                                                                                                                                                                                                                  TCTGCCGATGGCATGCTGACCTTCTGTGGCCCCAAGATCCAG
                                                                                                                                                                                                                                                                                                                                                                                      ATTGAGGTGCATGGAAAACATGAAGAGCGCCAGGATGAACATGGTTTCATCTCCAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCCTCGATGTGAAGCACTTCTCCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTT
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                                                                                                                                                                                                                                                                                TCATCTGATGGGGTCCTCACTGTGAATGGACCAAGGAAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                   ng; prostate; pancreas; carcin
gene therapy; antineoplastic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from cancer patients, used monitoring or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obata
                                                                                                                                        related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                          colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168
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                                                                                                                                                                                                                  DNA;
                                                                                                                                       gene sequence
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Pfreundschuh M,
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Pred. No. 8e
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                                                                                                                                       SEQ ID
                                                                                   carcinoma; and
lastic; Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 167
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M, Tureci O,
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                                                                                               antitumour; cancerous;
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products for the
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in U;
                                                                                   adenocarcinoma;
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18-SEP-2000;
20-SEP-2000;
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27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
28-SEP-2000;
29-SEP-2000;
29-SE
                  comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
                                                                                                                                                                                                              neoplastic agent. The method involves captures - neoplastic agent. The method involves captures - neoplastic activity, determining a change in to be tested for anti-neoplastic activity, determining a change in to be tested for activity, determining a change in the captures of at least one gene (I) of a signature gene set, where (I) expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (given in ABL6164) comprises a sequence (S) selected from 8447 sequences (Given in ABL6164) comprises a sequence (S) selected from 8447 sequences (Given in ABL6164) comprises a sequence (S) selected from 8447 sequences (Given in ABL6164) comprises a sequence (S) selected from 8447 sequences (Given in ABL6164) comprises (Given in ABL6164) comprises (Given in ABL6164) comprises (Given in ABL6164) comprises (Given in A
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05-JUN-2000;
18-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1; SEQ ID NO 3541; 44pp; English.
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Weaver Z
pancreatic
                                                                                                                                                                                                                                                                                                                                                                                           invention
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2000US-0234567P
2000US-0234924P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a gene
                                                                                                                                                                                                                                                                                                                                                        The method involves exposing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-neoplastic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of a signature gene
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adenocarcinoma,
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carcinoma,
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22-SEP-2000

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cytostatic;
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atic; gene therapy; antineopl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCTCGATGTGAAGCACTTCTCCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTT
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2000US-0209531P

2000US-0233617P

2000US-0234009P

2000US-0234034P

2000US-0234052P

2000US-0234567P

2000US-0234923P

2000US-0234923P

2000US-0234923P

2000US-0235077P

2000US-0235037P

2000US-0235638P

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                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US010838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ductal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                breast; ovary; oesophagus; kidney; thyroid;
te; pancreas; carcinoma; antitumour; cancerous;
apy; antineoplastic; Wilm's tumour; adenocarcin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
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C;
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Pred. No. 8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148
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d Wilm's
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28-SEP-2000;

28-SEP-2000;

28-SEP-2000;

29-SEP-2000;

29-SEP-2000;

02-OCT-2000;

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27-SEP-2000;
28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
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                                                                                                                                                                                                                                    2000US-0235840P.
2000US-0236028P.
2000US-0236032P.
2000US-0236033P.
2000US-0236119P.
2000US-0236111P.
2000US-0236842P.
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2000US-0237294P.
2000US-0237316P.
2000US-0237666P.
2000US-0237606P.
2000US-0237606P.
2000US-0237606P.
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Soppet Young T PE, Augustus Weaver Z ν, Σ, **3** Carter č, Ebner R, Endress G. Horrigan S

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing agent to be tested for anti-neoplastic activity, and in expression of a gene of a signature gene set. g cells to a determining t chemical ga change

Claim 1; SEQ ID NO 764; 44pp; English.

The present invention describes a method (M1) for screening for an antiCC neoplastic agent. The method involves exposing cells to a chemical agent
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95 identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC the coll carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

Sequence 691 BP; 168 A; 208 C; 148 G; 167 T; 0 U; 0 Other;

Similarity

33.2%;

Score 123.6; DB Pred. No. 8e-19;

DB

6;

Length

691;

Gaps

Query Match Best Local S Matches 183 197 10 CCCAGCTGGTTTGACACTGGACTCTCAGAGATGCGCCTGGAGAAGGACAGGTTCTCTGTC TTCCTCGATGTGAAGCACTTCTCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTT 129 CGCACCGTGCTGGACTCCCGGCATCTCTGAGGTTCGATCCGACCGGGGACAAGTTCGTCATC GTGGAGATCCACGGAAAGCACAACGAGCGCCAGGACGACCACGGCTACATTTCCCGTGAG AACCTGGATGTGAAGCACTTCTCCCCAGAGGAACTCAAAGTTAAGGTGTTGGGAGATGTG Conservative o ; Mismatches ; 99 Indels 0; 316 256 69 189

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                                                         Query Match
Best Local S
Matches 183
                                                                                                                                                                                    cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the used as diagnostic markers for the prediction or identification of the cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention. Note: The sequence data for this patent
                                                                                                                                                                                                                                                                                                        The present invention relates to methods of diagnosing breast cancer in patient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867-ABT11112, where a differential expression of the genes indicates breast
                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing breast cancer in a patient comprises detecting the level gene expression in cell or tissue samples, where a differential gen expression is indicative of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2001;
25-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; breast specific gene; breast cancer; differential expression;
cytostatic; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABT10966;
                                                                                                                   Sequence
                                                                                                                                                          did not form part of the printed specification, electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2002; 2002WO-US002176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABT10966 standard; cDNA;
                                                                                                                                             ftp.wipo.int/pub.published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-674803/72.
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                                                                                                                   691
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                                                           Conservative
                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0263757P.
2001US-0286090P.
2001US-0292517P.
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                                                                                                                 168 A;
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                                                                     33.2%;
                                                                                                                   208
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                                                                                                                                              pct_sequences
                                                        ; Score 123.6; pred. No. 8e-1 0; Mismatches
                                                                                                                   C; 148 G; 167 T; 0 U;
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                                                                        8e-19;
                                                                                     DB 6;
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                                                                                      Length 691;
                                                                                                                   0 Other;
                                                           Indels
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70

TTCCTCGATGTGAAGCACTTCTCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTT

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RESULT 12
ABK64671
ID ABK64
The methods are useful to present information identifying the expression level in a tissue or cells, by comparing the expression level of genes given in the specification in the tissue or cells to the level of expression of gene in the database, and displaying the expression levels of at least one gene in the tissue or cell sample compared to the expression level in BPH. Agents using (II) are useful for treating BPH or
                                                                                                                                                                                             from patients exhibiting different clinical states of prostate hyperplasia as compared to normal prostate tissue. (I) comprises detecting the expression levels of one or more genes in prostate cells from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the agent preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression profiles. (I) is useful for diagnosing the onset or progression of BPH. (II) is useful for identifying an agent that modulates the onset or progression of BPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 progression of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BPH. The method is based on changes in gene expression in BPH tissue isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
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05-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human benign prostatic hyperplasia gene #566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of diagnosing (I) the onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An OFF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of
                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                        Claim 1; SEQ ID NO 3891; 71pp + Sequence Listing; English.
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The present sequence is one of a large number of 5' ESTs derived f mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared

Claim 1; SEQ

ID NO 14942; 71pp + Sequence Listing;

English.

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herapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCAGCTGGTTTGACACTGGACTCTCAGAGATGCGCCTGGAGAAGGACAGGTTCTCTGTC 496
        SEQ
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     NO 14938;
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Pred. No. 8.2e-19;
0; Mismatches 99
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     Sequence
                                                            and chromosome
                                                                                                                                                                                                                           Giordano
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                                                                                tag (5' EST)
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               libraries. Such ESTs are not well suited for isolating CDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. ESTs are derived from mRNAs with intact 5' ends and can therefore be us to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 911 BP; 221 A; 260 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression and secretion vectors
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33; Conservative
                                                                                                                                                                                                                                       AACCTGGATGTGAAGCACTTCTCCCCAGAGGAACTCAAAGTTAAGGTGTTGGGAGATGTG
                                                                                                                                                                                                                                                             TTCCTCGATGTGAAGCACTTCTCCCCGGAGGACCTCACCGTGAAGGTGCAGGACGACTTT
                                                                                                                                                                                                                                                                                                                  CCCAGCTGGTTTGACACTGGACTCTCAGAGATGCGCCTGGAGAAGGACAGGTTCTCTGTC
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                                                                                                                                                           ATTGAGGTGCATGGAAAACATGAAGAGCGCCAGGATGAACATGGTTTCATCTCCAGGGAG
                                                                                                                                                                                                  GTGGAGATCCACGGAAAGCACGACGCCCAGGACGACCACGGCTACATTTCCCGTGAG
                                      TCTGCCGATGGCATGCTGACCTTCTGTGGCCCCAAGATCCAG
                                                                                                                TTCCACCGCCGCTACCGCCTGCCGTCCAACGTGGACCAGTCGGCCCTCTTTGCTCCCTG
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TCATCTGATGGGGTCCTCACTGTGAATGGACCAAGGAAACAG
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Pred. No. 8.2e-19;
0; Mismatches 99;
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